ANTISENSE MODULATION OF GFAT EXPRESSION

The present application claims priority under Title 35, United States Code, §119 to United States Provisional application Serial No. 60/419,268, filed October 17, 2002, which is incorporated by reference in its entirety as if written herein.

FIELD OF THE INVENTION

[001] The present invention provides compositions and methods for modulating the expression of Glutamine-fructose-6-phosphate amidotransferase (GFAT). In particular, this invention relates to antisense compounds, particularly oligonucleotides, specifically hybridizable with nucleic acids encoding Glutamine-fructose-6-phosphate amidotransferase. Such oligonucleotides have been shown to modulate the expression of Glutamine-fructose-6-phosphate amidotransferase.

BACKGROUND OF THE INVENTION

[002] Type 2 diabetes is a metabolic disease linked to obesity in the adult population. The growing incidence ranks Type 2 diabetes as one of the fastest growing diseases (40.3 million in 2000 global clinical incidence, annual growth rate of +4.9%). Yet, diabetes is neither adequately diagnosed (64% of the affected population diagnosed) nor treated. Current therapeutics for the treatment of Type 2 diabetes include insulin replacement, insulin secretagogues and insulin sensitizers. Despite introduction of the PPARgamma agonists, which improve insulin action in both liver and peripheral tissues, clinical experience demonstrates that plasma glucose levels of the treated population remain significantly above the non-diabetic level. Each of the currently available therapies has significant side effects. Hyperglycemia and poor glycemic control promote diabetic complications such as retinopathy, neuropathy, nephropathy, and increased risk of cardiovascular disease. Therapeutic agents which act at the fundamental defect(s) leading to insulin resistance should be more capable of normalizing blood glucose and providing

disease modification. No disease modifying agents have been registered for clinical use to date.

[003] It is now well established that abnormalities in insulin sensitive mechanisms and reduced secretion of insulin are causes of insufficient insulin activity in Type 2 diabetes. Insulin resistance is evident in patients prior to the onset of frank diabetes, which is diagnosed by elevated fasting blood glucose and a rise in HbA1c levels, indicating poor glycemic control. With recent advances in molecular biology, the cellular and molecular mechanisms underlying insulin resistance such as the insulin receptor structure and the mechanism of signal transduction downstream of the receptor have been investigated in detail. During the last decade, glucose transporter genes have been cloned and the relationship between mutations in the genes and the process of diabetes has been studied. However, the insulin, glucokinase, and mitochondrial gene abnormalities so far elucidated, taken together, account for not more than 1% of diabetes cases. While other gene abnormalities are to be revealed in the future, the environment and life style appear to be predominant drivers for a large percentage of the Type 2 diabetes cases. The correlation of diabetes with obesity, excessive nutrient availability and the lack of exercise has been amply documented as a primary cause of insulin resistance and progression to Type 2 diabetes. The ability to treat Type 2 diabetes by diet, exercise, and weight loss demonstrates the contribution of these causal factors. However, poor patient compliance and an inability to modify diet, reduce weight, or increase activity levels accounts for the high percentage of Type 2 diabetics who cannot control their diabetes without therapeutic intervention.

[004] Current therapeutics for the treatment of Type 2 diabetes include insulin replacement, insulin secretagogues and insulin sensitizers. Despite introduction of the PPARgamma agonists, which improve insulin action in both liver and peripheral tissues, clinical experience demonstrates that plasma glucose levels of the treated population remain significantly above the non-diabetic level. Moreover, each of the currently available therapies has significant side effects including weight gain, dose-limiting edema, and potential for hepatic toxicity. Furthermore, attempts at second-generation PPARgamma agonist that include PPARalpha activation (e.g., JTT-501,

NN6222) have met with difficulties that have precluded clinical development. In recent years, antidiabetic agents quite differing from the conventional oral hypoglycemic agents in the mechanism of action, such as the α-glycosidase inhibitors acarbose and voglibose (*Diabetes Frontier*, 3, 557-564 (1992); *Drugs*, 46, 1025-1054 (1994); Igaku no Ayumi, 149, 591-618 (1989); Rinsho to Kenkyu (*Japan. J. Clinics Exper. Med.*), 67, 219-233 (1990); Rinsho to Kenkyu, 69, 919-932 (1992); Rinshoi (*Clinical Medicine*), 21 (supplement), 578-587 (1995)) and the insulin resistance improving agents, troglitazone and pioglitazone, (*Diabetes*, 37, 1549-1558 (1998); Rinsho Iyaku, 9 (supplement 3), 127-150 (1993); *New Engl. J. Med.*, 331, 1188-1193 (1994); *Atarashii Tonyobyo Chiryoyaku (New Antidiabetics)* (edited by Yoshio Goto), published by Iyaku Journal Co., Osaka, (1994)) have been developed. Meanwhile, in the United States, a biguanide derivative was approved in 1996 as an antidiabetic for general prescription (*New Engl. J. Med.*, 333, 541-549 (1995); *Diabetes Spectrum*, 8, 194-197 (1995)). The above-mentioned drugs, unlike sulfonylureas (SUs), which have been used for many years in routine medical care, produce a hypoglycemic effect without promoting insulin secretion from β cells of the pancreas.

[005] It is considered, at present, that there are nine mechanisms through which antidiabetics might be able to improve insulin resistance as follows: (1) activation of insulin receptor kinase, (2) promotion of translocation of glucose transporters, (3) correction of the action of the rate-limiting enzyme involved in glucose metabolism and correction of abnormalities in glucose metabolism, (4) inhibition of gluconeogenesis in liver, (5) promotion of glucose uptake by liver, (6) enhancement of glycogenesis in liver, (7) reduction in blood lipid level, (8) decrease in gluconeogenesis in liver as resulting from the reduction in blood lipid level, and (9) enhancement of insulin sensitivity as resulting from the reduction in blood lipid level.

[006] A growing body of data implicates the hexosamine pathway as a primary energy sensor in mammals, and demonstrates that an increased rate of hexosamine biosynthesis produces profound insulin resistance. GFAT is an important enzyme catalyzing the conversion of fructose-6- phosphate to glucosamine-6-phosphate, which is the rate-limiting step in the hexosamine

biosynthesis pathway. Inhibitors of GFAT activity are thought to promote glucose influx by cells and thereby reducing the blood glucose level. Therefore, these inhibitors are expected to be of use as antidiabetics. Their mechanism of action is thought to be associated with the process (2) or (5) mentioned above.

[007] While the hexosamine biosynthesis pathway metabolizes glucosamine-6- phosphate to UDP-N-acetylglucosamine, CMP-N-acetylneuraminic acid, etc., those metabolic intermediates are thought to be utilized as precursors for glycosylation of proteins or as essential substrates for the synthesis of proteoglycans and gangliosides.

[008] Insulin activates its signal transduction pathway through binding insulin receptor and translocates glucose transporters (GLUT4 etc.) pooled within cells to the cell membrane resulting in increasing glucose influx. Glucose is metabolized by glycolysis pathway and ATP is accumulated as an energy source. When the influx of glucose is excessive, however, or when glucose metabolism is diverted away from the glycolytic enzyme phosphofructokinase and into the hexosamine biosynthetic pathway, increased fructose-6-phosphate enters the hexosamine biosynthesis pathway and is converted to glucosamine-6-phosphate catalyzed by GFAT. Physiological increases in the rate of GFAT biosynthesis of glucosamine-6-phosphate results in an accumulation of the pathway end-product, UDP-N-acetylglucosamine. Although detailed mechanisms remain unknown, several observations indicate that metabolites of glucosamine-6-phosphate prevent glucose transporters from translocating to cell membrane, resulting in reducing cellular glucose influx (*FASEB J.*, 5, 3031-3036 (1991); *Diabetologia*, 38, 518-524 (1995); *J. Biol. Chem.*, 266, 10115-10161 (1991): *J. Biol. Chem.*, 266, 4706-4712 (1991); *Endocrinology*, 136, 2809-2816 (1995)).

[009] Therefore, the hexosamine biosynthesis pathway is considered to control the influx of glucose by a feed-back manner. GFAT is the rate- limiting enzyme in this pathway. GFAT activity is also known to be generally high in patients with Type 2 diabetes and is considered to be one of the causes of high blood glucose levels (*Diabetes*, 45, 302-307 (1996)).

[0010] Hypoglycemic agents, such as inhibitors of GFAT activity, whose action is mainly directed to some other tissues than pancreas invariably,

improve insulin resistance in target tissues. These agents have some clinical merits in addition to their hypoglycemic activity, because of their secondary effects. When used in combination with other drugs, they are highly effective and have very bright prospects before them.

[0011] Recently a human GFAT-1 gene has been cloned (*J. Biol. Chem.*, 267, 25208- 25212 (1992)). The gene product is a 77 kDa protein composed of 681 amino acid residues. GFAT-1 genes have been cloned from other animal species as well. For example, a murine GFAT-1 is highly homologous to the human GFAT-1 (91% at the nucleotide level and 98.6% at the amino acid level), hence it is considered to be the counterpart of the human GFAT-1 (*Gene*, 140, 289-290 (1994)). In addition, a yeast GFAT-1 (*J. Biol. Chem.*, 264, 8753-8758 (1989)) and a Escherichia coli -derived GFAT (*Biochem. J.*, 224, 779-815 (1984)) have also been reported, each having high homology with the human GFAT.

[0012] Recently human and mouse full-length cDNAs of a novel subtype of GFAT which was designated GFAT-2 (the previously reported GFAT was named GFAT-1) has been cloned. Both the human and the mouse GFAT-2 proteins are composed of 682 amino acids of approximately 77.0 kDa. At the amino acid level, homologies between the human GFAT-1 and GFAT-2, between the mouse GFAT-1 and GFAT-2, and between the human GFAT-2 and the mouse GFAT-2 were 75.6, 74.7, and 97.2%, respectively. GFAT-1 is more highly expressed in the placenta, pancreas, and testis than GFAT-2; GFAT-2 was expressed throughout the central nervous system, especially in the spinal cord, but GFAT-1 expression was weak. The locus was mapped to human chromosome 5q and mouse chromosome 11, where a synteny between the two species has been known.

[0013] GFAT-1 is ubiquitous, whereas GFAT-2 is expressed mainly in the central nervous system. In the course of developing a competitive reverse transcriptase-polymerase chain reaction assay, we noted that GFAT-1 cDNA from muscle but not from other tissues migrated as a doublet. Subsequent cloning and sequencing revealed two GFAT-1 mRNAs in both mouse and human skeletal muscles. The novel GFAT-1 mRNA (GFAT-1Alt [muscle selective variant of GFAT-1]) is likely a splice variant. It is identical to GFAT-1

except for a 48 or 54 bp insert in the mouse and human, respectively, at nucleotide position 686 of the coding sequence, resulting in a 16 or 18 amino acid insert at position 229 of the protein. GFAT-1Alt is the predominant GFAT-1 mRNA in mouse hindlimb muscle, is weakly expressed in the heart, and is undetectable in the brain, liver, kidney, lung, intestine, spleen, and 3T3-L1 adipocytes. In humans, it is strongly expressed in skeletal muscle but not in the brain. GFAT-1 and GFAT-1Alt expressed by recombinant adenovirus infection in COS-7 cells displayed robust enzyme activity and kinetic differences. The apparent K(m) of GFAT-1Alt for fructose-6-phosphate was approximately twofold higher than that of GFAT-1, whereas K(i) for UDP-N-acetylglucosamine was approximately fivefold lower. Muscle insulin resistance is a hallmark and predictor of type 2 diabetes. Variations in the expression of GFAT isoforms in muscle may contribute to predisposition to insulin resistance.

[0014] Evidence has accumulated that glucose flux through the hexosamine biosynthetic pathway may provide a nutrient-sensing hyperglycosylation that is responsible for glucose-induced insulin resistance (Rossetti, L. (2000) *Endocrinology* 141, 1922-1925). For example, it has been reported that targeted overexpression of the rate-limiting enzyme for hexosamine synthesis in the striated muscle and fat of transgenic mice leads to insulin resistance (Hebert, L. F. J., et al., (1996) *J. Clin. Invest.* 98, 930-936). This insulin resistance was phenotypically similar to that observed in human type 2 diabetes. Specifically, the insulin resistance was characterized by decreased insulin-dependent recruitment of GLUT4 to the plasma membrane and was reversed by the thiazolidinedione antidiabetic drug troglitazone (Cooksey, R. C., et al., (1999) *Endocrinology* 140, 1151-1157). Significantly, glucose also up-regulates the ob gene via the hexosamine pathway, which leads to enhanced leptin expression (Wang, J., et al., (1998) *Nature* (London) 393, 684-688; McClain, D. A., et al., (2000) *Endocrinology* 141, 1999-2002). Insulin resistance caused by free fatty acids has also been suggested to be sensed through the hexosamine pathway (Hawkins, M., et al., (1997) *J. Clin. Invest.* 99, 2173-2282). These data support the function of the hexosamine biosynthetic pathway as a central nutrient sensor for both glucose and free fatty acids.

[0015] How the products of the hexosamine pathway might exert nutrient sensing or regulate signal transduction is not known. A leading hypothesis suggests that the terminal metabolite of the pathway, UDP-GlcNAc, is used as a substrate by the recently cloned O-linked GlcNAc transferase (OGT) (Lubas, W. A., (1997) *J. Biol. Chem.* 272, 9316-9324; Kreppel, L. K., et al., (1997) *J. Biol. Chem.* 272, 9308-9315; Hanover, J. A. (2001) *FASE*B J. 15, 1865-1876; Wells, L., et al., (2001) *Science* 291, 2376-2378). O-linked glycosylation by GlcNAc modifies the serine and threonine residues of cytosolic and nuclear proteins and, like phosphorylation, can change the function of such proteins as Sp1 and endothelial nitrogen oxide synthase (Yang, X., et al., (2001) *Proc. Natl. Acad. Sci. USA* 98, 6611-6616; Du, X. L., et al., (2001) *J. Clin. Invest.* 108, 1341-1348).

[0016] Antisense technology is emerging as an effective means for reducing the expression of specific gene products and may therefore prove to be uniquely useful in a number of therapeutic, diagnostic, and research applications for the modulation of GFAT expression. Systemically administered antisense has been shown to accumulate and have its effect predominately in liver and to a lessor extent in fat (R. S. Geary, et al., *Curr.Opin.Investig.Drugs* Volume 2, Issue 4, pp. 562-573). It would be useful to modulate GFAT-1 expression in liver and fat, making these two insulin target organs more insulin sensitive and thus attenuating the severity of diabetes. If in the future it becomes possible to deliver antisense to striated muscle, another insulin sensitive tissue, modulation of GFAT-1Alt may provide additional benefit in the treatment of diabetic hyperglycemia.

SUMMARY OF THE INVENTION

[0017] The present invention is directed to antisense compounds, particularly oligonucleotides, which are targeted to a nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase (GFAT or GFA), also referred to as glutamine-fructose-6-phosphate transaminase (GFPT), Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1 (EC 2.6.1.16), Hexosephosphate aminotransferase 1, D-fructose-6- phosphate

amidotransferase, which modulate the expression of GFAT. Pharmaceutical and other compositions comprising the antisense compounds of the invention are also provided. Further provided are methods of modulating the expression of GFAT in cells or tissues comprising contacting said cells or tissues with one or more of the antisense compounds or compositions of the invention. Further provided are methods of treating an animal, particularly a human, suspected of having or being prone to a disease or condition associated with expression of GFAT by administering a therapeutically or prophylactically effective amount of one or more of the antisense compounds or compositions of the invention.

BRIEF DESCRIPTION OF THE FIGURES

[0018] Figure 1 shows the human GFAT-1 amino acid sequence and the nucleic acid encoding such (GenBank accession number NM_002056).

DETAILED DESCRIPTION OF THE INVENTION

[0020] The present invention employs oligomeric antisense compounds, particularly oligonucleotides, for use in modulating the function of nucleic acid molecules encoding GFAT, ultimately modulating the amount of GFAT produced. This is accomplished by providing antisense compounds, which specifically hybridize with one or more nucleic acids encoding GFAT. As used herein, "GFAT" includes glutamine-fructose-6-phosphate aminotransferase 1 (GFAT-1) (*J. Biol. Chem.*, 267, 25208- 25212 (1992)), glutamine-fructose-6-phosphate aminotransferase 1 Alt (GFAT-1Alt) (DeHaven et. al. *Diabetes* 2001 Nov, 50(11):2419-24) and glutamine-fructose-6-phosphate aminotransferase 2 (GFAT-2) (WO 00/37617). In a preferred embodiment the oligomeric antisense oligonucleotides modulate the function of nucleic acid molecules encoding human GFAT-1. As used herein, the terms "target nucleic acid" and "nucleic acid encoding GFAT" encompass DNA encoding GFAT, RNA (including pre-mRNA and mRNA) transcribed from such DNA, and also cDNA derived from such RNA. The specific hybridization of an oligomeric compound with its target nucleic acid interferes with the normal function of the nucleic acid. This

modulation of function of a target nucleic acid by compounds, which specifically hybridize to it, is generally referred to as "antisense". The functions of DNA to be interfered with include replication and transcription. The functions of RNA to be interfered with include all vital functions such as, for example, translocation of the RNA to the site of protein translation, translation of protein from the RNA, splicing of the RNA to yield one or more mRNA species, and catalytic activity which may be engaged in or facilitated by the RNA. The overall effect of such interference with target nucleic acid function is modulation of the expression of GFAT. In the context of the present invention, "modulation" means either an increase (stimulation) or a decrease (inhibition) in the expression of a gene. In the context of the present invention, inhibition is the preferred form of modulation, of gene expression and mRNA is a preferred target.

[0021] It is preferred to target specific nucleic acids for antisense. "Targeting" an antisense compound to a particular nucleic acid, in the context of this invention, is a multistep process. The process usually begins with the identification of a nucleic acid sequence whose function is to be modulated. This may be, for example, a cellular gene (or mRNA transcribed from the gene) whose expression is associated with a particular disorder or disease state, or a nucleic acid molecule from an infectious agent. In the present invention, the target is a nucleic acid molecule encoding GFAT. The targeting process also includes determination of a site or sites within this gene for the antisense interaction to occur such that the desired effect, e.g., detection or modulation of expression of the protein, will result. Within the context of the present invention, a preferred intragenic site is the region encompassing the translation initiation or termination codon of the open reading frame (ORF) of the gene. Since, as is known in the art, the translation initiation codon is typically 5'-AUG (in transcribed mRNA molecules; 5'-ATG in the corresponding DNA molecule), the translation initiation codon is also referred to as the "AUG codon," the "start codon" or the "AUG start codon". A minority of genes have a translation initiation codon having the RNA sequence 5'-GUG, 5'-UUG or 5'-CUG, and 5'-AUA, 5'-ACG and 5'-CUG have been shown to function in vivo. Thus, the terms "translation initiation codon" and "start codon" can encompass

many codon sequences, even though the initiator amino acid in each instance is typically methionine (in eukaryotes) or formylmethionine (in prokaryotes). It is also known in the art that eukaryotic and prokaryotic genes may have two or more alternative start codons, any one of which may be preferentially utilized for translation initiation in a particular cell type or tissue, or under a particular set of conditions. In the context of the invention, "start codon" and "translation initiation codon" refer to the codon or codons that are used in vivo to initiate translation of an mRNA molecule transcribed from a gene encoding GFAT, regardless of the sequence(s) of such codons.

[0022] It is also known in the art that a translation termination codon (or "stop codon") of a gene may have one of three sequences, i.e. 5'-UAA, 5'-UAG and 5'-UGA (the corresponding DNA sequences are 5'-TAA, 5'-TAG and 5'-TGA, respectively). The terms "start codon region" and "translation initiation codon region "refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation initiation codon. Similarly, the terms "stop codon region" and "translation termination codon region "refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation termination codon.

[0023] The open reading frame (ORF) or "coding region," which is known in the art to refer to the region between the translation initiation codon and the translation termination codon, is also a region which may be targeted effectively. Other target regions include the 5' untranslated region (5'UTR), known in the art to refer to the portion of an mRNA in the 5' direction from the translation initiation codon, and thus including nucleotides between the 5' cap site and the translation initiation codon of an mRNA or corresponding nucleotides on the gene, and the 3' untranslated region (3'UTR), known in the art to refer to the portion of an mRNA in the 3' direction from the translation termination codon, and thus including nucleotides between the translation termination codon and 3' end of an mRNA or corresponding nucleotides on the gene. The 5' cap of an mRNA comprises an N7-methylated guanosine residue joined to the 5'-most residue of the mRNA via a 5'-5' triphosphate linkage. The 5' cap region of an mRNA is considered to include the 5' cap structure itself as

well as the first 50 nucleotides adjacent to the cap. The 5' cap region may also be a preferred target region.

[0024] Although some eukaryotic mRNA transcripts are directly translated, many contain one or more regions, known as "introns," which are excised from a transcript before it is translated. The remaining (and therefore translated) regions are known as "exons" and are spliced together to form a continuous mRNA sequence. mRNA splice sites, i.e., intron-exon junctions, may also be preferred target regions, and are particularly useful in situations where aberrant splicing is implicated in disease, or where an overproduction of a particular mRNA splice product is implicated in disease. Aberrant fusion junctions due to rearrangements or deletions are also preferred targets. It has also been found that introns can also be effective, and therefore preferred, target regions for antisense compounds targeted, for example, to DNA or pre-mRNA.

[0025] Once one or more target sites have been identified, oligonucleotides are chosen which are sufficiently complementary to the target, i.e., hybridize sufficiently well and with sufficient specificity, to give the desired effect.

[0026] In the context of this invention, "hybridization" means hydrogen bonding, which may be Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding, between complementary nucleoside or nucleotide bases. For example, adenine and thymine are complementary nucleobases, which pair through the formation of hydrogen bonds. "Complementary," as used herein, refers to the capacity for precise pairing between two nucleotides. For example, if a nucleotide at a certain position of an oligonucleotide is capable of hydrogen bonding with a nucleotide at the same position of a DNA or RNA molecule, then the oligonucleotide and the DNA or RNA are considered to be complementary to each other at that position. The oligonucleotide and the DNA or RNA are complementary to each other when a sufficient number of corresponding positions in each molecule are occupied by nucleotides which can hydrogen bond with each other. Thus, "specifically hybridizable" and "complementary" are terms which are used to indicate a sufficient degree of complementarity or precise pairing such that stable and specific binding occurs between the oligonucleotide and the DNA or RNA target. It is understood in the art that the sequence of an antisense compound need not be 100%

complementary to that of its target nucleic acid to be specifically hybridizable. An antisense compound is specifically hybridizable when binding of the compound to the target DNA or RNA molecule interferes with the normal function of the target DNA or RNA to cause a loss of utility, and there is a sufficient degree of complementarity to avoid non-specific binding of the antisense compound to non-target sequences under conditions in which specific binding is desired, i.e., under physiological conditions in the case of in vivo assays or therapeutic treatment, and in the case of in vitro assays, under conditions in which the assays are performed.

[0027] Antisense compounds are commonly used as research reagents and diagnostics. For example, antisense oligonucleotides, which are able to inhibit gene expression with exquisite specificity, are often used by those of ordinary skill to elucidate the function of particular genes. Antisense compounds are also used, for example, to distinguish between functions of various members of a biological pathway. Antisense modulation has, therefore, been harnessed for research use.

[0028] The specificity and sensitivity of antisense is also harnessed by those of skill in the art for therapeutic uses. Antisense oligonucleotides have been employed as therapeutic moieties in the treatment of disease states in animals and man. Antisense oligonucleotides have been safely and effectively administered to humans and numerous clinical trials are presently underway. It is thus established that oligonucleotides can be useful therapeutic modalities that can be configured to be useful in treatment regimes for treatment of cells, tissues and animals, especially humans. In the context of this invention, the term "oligonucleotide" refers to an oligomer or polymer of ribonucleic acid (RNA) or deoxyribonucleic acid (DNA) or mimetics thereof. This term includes oligonucleotides composed of naturally occurring nucleobases, sugars and covalent internucleoside (backbone) linkages as well as oligonucleotides having non-naturally occurring portions which function similarly. Such modified or substituted oligonucleotides are often preferred over native forms because of desirable properties such as, for example, enhanced cellular uptake, enhanced affinity for nucleic acid target and increased stability in the presence of nucleases.

[0029] While antisense oligonucleotides are a preferred form of antisense compound, the present invention comprehends other oligomeric antisense compounds, including but not limited to oligonucleotide mimetics such as are described below. The antisense compounds in accordance with this invention preferably comprise from about 8 to about 30 nucleobases (i.e. from about 8 to about 30 linked nucleo sides). Particularly preferred antisense compounds are antisense oligonucleotides, even more preferably those comprising from about 12 to about 25 nucleobases. As is known in the art, a nucleoside is a base-sugar combination. The base portion of the nucleoside is normally a heterocyclic base. The two most common classes of such heterocyclic bases are the purines and the pyrimidines. Nucleotides are nucleosides that further include a phosphate group covalently linked to the sugar portion of the nucleoside. For those nucleosides that include a pentofuranosyl sugar, the phosphate group can be linked to either the 2', 3' or 5' hydroxyl moiety of the sugar. In forming oligonucleotides, the phosphate groups covalently link adjacent nucleosides to one another to form a linear polymeric compound. In turn the respective ends of this linear polymeric structure can be further joined to form a circular structure, however, open linear structures are generally preferred. Within the oligonucleotide structure, the phosphate groups are commonly referred to as forming the internucleoside backbone of the oligonucleotide. The normal linkage or backbone of RNA and DNA is a 3' to 5' phosphodiester linkage.

[0030] Specific examples of preferred antisense compounds useful in this invention include oligonucleotides containing modified backbones or non-natural internucleoside linkages. As defined in this specification, oligonucleotides having modified backbones include those that retain a phosphorus atom in the backbone and those that do not have a phosphorus atom in the backbone. For the purposes of this specification, and as sometimes referenced in the art, modified oligonucleotides that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides.

[0031] Preferred modified oligonucleotide backbones include, for example, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl

phosphonates including 3'alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts and free acid forms are also included.

[0032] Representative United States patents that teach the preparation of the above phosphorus-containing linkages include, but are not limited to, U.S. 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,196; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455,233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563,253; 5,571,799; 5,587,361; and 5,625,050, each of which is herein incorporated by reference.

[0033] Preferred modified oligonucleotide backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH_2 component parts.

[0034] Representative United States patents that teach the preparation of the above oligonucleosides include, but are not limited to, U.S. 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,264,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,610,289; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; and 5,677,439, ach of which is herein incorporated by reference.

[0035] In other preferred oligonucleotide mimetics, both the sugar and the internucleoside linkage, i.e., the backbone, of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound, an oligonucleotide mimetic that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. Representative United States patents that teach the preparation of PNA compounds include, but are not limited to, U.S. 5,539,082; 5,714,331; and 5,719,262, each of which is herein incorporated by reference. Further teaching of PNA compounds can be found in Nielsen et al., *Science*, 1991, 254, 1497-1500.

[0036] Most preferred embodiments of the invention are oligonucleotides with phosphorothioate backbones and oligonucleosides with heteroatom backbones, and in particular -CH_2-NH-O-CH_2-, -CH_2-N (CH_3) -O-CH_2- [known as a methylene (methylimino) or MMI backbone], - CH_2-O-N (CH_3) -CH_2-, - $CH_2N(CH_3)$-$N(CH_3)$-CH_2- and -O-$N(CH_3)$-CH_2-CH_2- [wherein the native phosphodiester backbone is represented as -O-P-O-CH_2-] of the above referenced U.S. patent 5,489,677, and the amide backbones of the above referenced U.S. patent 5,602,240. Also preferred are oligonucleotides having morpholino backbone structures of the above-referenced U.S. patent 5,034,506.

[0037] Modified oligonucleotides may also contain one or more substituted sugar moieties. Preferred oligonucleotides comprise one of the following at the 2' position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C_1 to C_{10} alkyl or C_2 to C_{10} alkenyl and alkynyl. Particularly preferred are $O[(CH_2)_nO]_mCH_3$, $O(CH_2)_n,OCH_3$, $O(CH_2)_nNH_2$, $O(CH_2)_nCH_3$, $O(CH_2)_nONH_2$, and $O(CH_{2n}ON[(CH_2)_nCH_3)]_2$ where n and m are from 1 to about 10. Other preferred oligonucleotides comprise one of the following at the 2' position: C_1 to C_{10}, (lower alkyl, substituted lower alkyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH_3, OCN, Cl, Br, CN, CF_3, OCF_3, $SOCH_3$,

SO_2CH_3, $ON0_2$, NO_2, N_3, NH_2, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. A preferred modification includes 2' -methoxyethoxy (2' -O-$CH_2CH_2OCH_3$, also known as 2'-O- (2-methoxyethyl) or 2'-MOE) (Martin et al., *Helv. Chim. Acta*, 1995, 78, 486-504) i.e., an alkoxyalkoxy group. A further preferred modification includes 2'-dimethylaminooxyethoxy, i.e., a $O(CH_2)_2ON(CH_3)_2$ group, also known as 2'-DMAOE, as described in examples herein below, and 2'-dimethylaminoethoxyethoxy (also known in the art as 2'-O-dimethylaminoethoxyethyl or 2'-DMAEOE), i.e., 2'-O-CH_2-O-CH_2-N $(CH_2)_2$, also described in examples herein below.

[0038] Other preferred modifications include 2'-methoxy (2'-O CH_3), 2'-aminopropoxy (2'-O CH_2 CH_2 CH_2NH_2) and 2'-fluoro (2'-F). Similar modifications may also be made at other positions on the oligonucleotide, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Oligonucleotides may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar. Representative United States patents that teach the preparation of such modified sugar structures include, but are not limited to, U.S. 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; and 5,700,920, each of which is herein incorporated by reference in its entirety.

[0039] Oligonucleotides may also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-

thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylquanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Further nucleobases include those disclosed in United States Patent No. 3,687,808, those disclosed in *The Concise Encyclopedia Of Polymer Science And Engineering*, pages 858-859, Kroschwitz, J.I., ed. John Wiley & Sons, 1990, those disclosed by Englisch et al., *Angewandte Chemie*, International Edition, 1991, 30, 613, and those disclosed by Sanghvi, Y.S., Chapter 15, *Antisense Research and Applications*, pages 289-302, Crooke, S.T. and Lebleu, B. ed., CRC Press, 1993. Certain of these nucleobases are particularly useful for increasing the binding affinity of the oligomeric compounds of the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2°C (Sanghvi, Y.S., Crooke, S.T. and Lebleu, B., eds, *Antisense Research and Applications*, CRC Press, Boca Raton, 1993, pp. 276-278) and are presently preferred base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications.

[0040] Representative United States patents that teach the preparation of certain of the above noted modified nucleobases as well as other modified nucleobases include, but are not limited to, the above noted U.S. 3,687,808, as well as U.S. 4,845,205; 5,130,302; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,12', 5,596,091; 5,614,617; 5,750,692, and 5,681,941, each of which is herein incorporated by reference.

[0041] Another modification of the oligonucleotides of the invention involves chemically linking to the oligonucleotide one or more moieties or conjugates, which enhance the activity, cellular distribution, or cellular uptake of the oligonucleotide. Such moieties include but are not limited to lipid

moieties such as a cholesterol moiety (Letsinger et al., *Proc. Natl. Acad. Sci. USA*, 1989, 86, 6553-6556), cholic acid (Manoharan et al., *Bioorg. Med. Chem. Let.*, 1994, 4, 1053-1060), a thioether, e.g., hexyl-S-tritylthiol (Manoharan et al., *Ann. N.Y. Acad. Sci.*, 1992, 660, 306-309; Manoharan et al., *Bioorg. Med. Chem. Let.*, 1993, 3, 2765-2770), a thiocholesterol (Oberhauser et al., *Nucl. Acids Res.*, 1992, 20, 533-538), an aliphatic chain, e.g., dodecandiol or undecyl residues (Saison-Behmoaras et al., *EMBO J.*, 1991, 10, 1111-1118; Kabanov et al., *FEBS Lett.*, 1990, 259, 327-330; Svinarchuk et al., *Biochimie*, 1993, 75, 49-54), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan et al., *Tetrahedron Lett.*, 1995, 36, 3651-3654; Shea et al., *Nucl. Acids Res.*, 1990, 18, 3777-3783), a polyamine or a polyethylene glycol chain (Mancharan et al., *Nucleosides & Nucleotides*, 1995, 14, 969-973), or adamantane acetic acid (Manoharan et al., *Tetrahedron Lett.*, 1995, 36, 3651-3654), a palmityl moiety (Mishra et al., *Biochim. Biophys. Acta*, 1995, 1264, 229-237), or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety (Crooke et al., *J. Pharmacol. Exp. Ther.*, 1996, 277, 923-937).

[0042] Representative United States patents that teach the preparation of such oligonucleotide conjugates include, but are not limited to, U.S. 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538; 5,578,717, 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391,723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928 and 5,688,941, each of which is herein incorporated by reference.

[0043] It is not necessary for all positions in a given compound to be uniformly modified, and in fact more than one of the aforementioned modifications may be incorporated in a single compound or even at a single nucleoside within an oligonucleotide. The present invention also includes antisense compounds, which are chimeric compounds. "Chimeric" antisense

compounds or "chimeras," in the context of this invention, are antisense compounds, particularly oligonucleotides, which contain two or more chemically distinct regions, each made up of at least one monomer unit, i.e., a nucleotide in the case of an oligonucleotide compound. These oligonucleotides typically contain at least one region wherein the oligonucleotide is modified so as to confer upon the oligonucleotide increased resistance to nuclease degradation, increased cellular uptake, and/or increased binding affinity for the target nucleic acid. An additional region of the oligonucleotide may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNase H is a cellular endonuclease, which cleaves the RNA strand of RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of oligonucleotide inhibition of gene expression. Consequently, comparable results can often be obtained with shorter oligonucleotides when chimeric oligonucleotides are used, compared to phosphorothioate deoxyoligonucleotides hybridizing to the same target region. Cleavage of the RNA target can be routinely detected by gel electrophoresis and, if necessary, associated nucleic acid hybridization techniques known in the art.

[0044] Chimeric antisense compounds of the invention may be formed as composite structures of two or more oligonucleotides, modified oligonucleotides, oligonucleosides and/or oligonucleotide mimetics as described above. Such compounds have also been referred to in the art as hybrids or gapmers. Representative United States patents that teach the preparation of such hybrid structures include, but are not limited to, U.S. 5,013,830; 5,149,797; 5,220,007; 5,256,775; 5,366,878; 5,403,711; 5,491,133; 5,565,350; 5,623,065; 5,652,355; 5,652,356; and 5,700,922, each of which is herein incorporated by reference in its entirety.

[0045] The antisense compounds used in accordance with this invention may be conveniently, and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including, for example, Applied Biosystems (Foster City, CA). Any other means for such synthesis known in the art may additionally or alternatively be

employed. It is well known to use similar techniques to prepare oligonucleotides such as the phosphorothioates and alkylated derivatives.

[0046] The antisense compounds of the invention are synthesized in vitro and do not include antisense compositions of biological origin, or genetic vector constructs designed to direct the in vivo synthesis of antisense molecules. The compounds of the invention may also be admixed, encapsulated, conjugated or otherwise associated with other molecules, molecule structures or mixtures of compounds, as for example, liposomes, receptor targeted molecules, oral, rectal, topical or other formulations, for assisting in uptake, distribution and/or absorption. Representative United States patents that teach the preparation of such uptake, distribution and/or absorption assisting formulations include, but are not limited to, U.S. 5,108,921; 5,354,844; 5,416,016; 5,459,127; 5,521,291; 5,543,158; 5,547,932; 5,583,020; 5,591,721; 4,426,330; 4,534,899; 5,013,556; 5,108,921; 5,213,804; 5,227,170; 5,264,221; 5,356,633; 5,395,619; 5,416,016; 5,417,978; 5,462,854; 5,469,854; 5,512,295; 5,527,528; 5,534,259; 5,543,152; 5,556,948; 5,580,575; and 5,595,756, each of which is herein incorporated by reference.

[0047] The antisense compounds of the invention encompass any pharmaceutically acceptable salts, esters, or salts of such esters, or any other compound which, upon administration to an animal including a human, is capable of providing (directly or indirectly) the biologically active metabolite or residue thereof. Accordingly, for example, the disclosure is also drawn to prodrugs and pharmaceutically acceptable salts of the compounds of the invention, pharmaceutically acceptable salts of such prodrugs, and other bioequivalents.

[0048] The term "prodrug" indicates a therapeutic agent that is prepared in an inactive form that is converted to an active form (i.e., drug) within the body or cells thereof by the action of endogenous enzymes or other chemicals and/or conditions. In particular, prodrug versions of the oligonuclectides of the invention are prepared as SATE [(S-acetyl-2-thioethyl) phosphate] derivatives according to the methods disclosed in WO 93/24510 to Gosselin et al., published December 9, 1993 or in WO 94/26764 to Imbach et al.

[0049] The term "pharmaceutically acceptable salts" refers to physiologically and pharmaceutically acceptable salts of the compounds of the invention: i.e., salts that retain the desired biological activity of the parent compound and do not impart undesired toxicological effects thereto.

[0050] Pharmaceutically acceptable base addition salts are formed with metals or amines, such as alkali and alkaline earth metals or organic amines. Examples of metals used as cations are sodium, potassium, magnesium, calcium, and the like. Examples of suitable amines are N, N'-dibenzylethylenediamine, chloroprocaine, choline, diethanolamine, dicyclohexylamine, ethylenediamine, N-methylglucamine, and procaine (see, for example, Berge et al., "Pharmaceutical Salts," *J. of Pharma Sci.*, 1977, 66, 119). The base addition salts of said acidic compounds are prepared by contacting the free acid form with a sufficient amount of the desired base to produce the salt in the conventional manner. The free acid form may be regenerated by contacting the salt form with an acid and isolating the free acid in the conventional manner. The free acid forms differ from their respective salt forms somewhat in certain physical properties such as solubility in polar solvents, but otherwise the salts are equivalent to their respective free acid for purposes of the present invention. As used herein, a "pharmaceutical addition salt" includes a pharmaceutically acceptable salt of an acid form of one of the components of the compositions of the invention. These include organic or inorganic acid salts of the amines. Preferred acid salts are the hydrochlorides, acetates, salicylates, nitrates and phosphates. Other suitable pharmaceutically acceptable salts are well known to those skilled in the art and include basic salts of a variety of inorganic and organic acids, such as, for example, with inorganic acids, such as for example hydrochloric acid, hydrobromic acid, sulfuric acid or phosphoric acid; with organic carboxylic, sulfonic, sulfo or phospho acids or N-substituted sulfamic acids, for example acetic acid, propionic acid, glycolic acid, succinic acid, maleic acid, hydroxymaleic acid, methylmaleic acid, fumaric acid, malic acid, tartaric acid, lactic acid, oxalic acid, gluconic acid, glucaric acid, glucuronic acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, salicylic acid, 4-aminosalicylic acid, 2-phenoxybenzoic acid, 2-acetoxybenzoic acid, embonic acid, nicotinic acid or isonicotinic acid; and with

amino acids, such as the 20 alpha-amino acids involved in the synthesis of proteins in nature, for example glutamic acid or aspartic acid, and also with phenylacetic acid, methanesulfonic acid, ethanesulfonic acid, 2-hydroxyethanesulfonic acid, ethane-1,2-disulfonic acid, benzenesulfonic acid, 4-methylbenzenesulfoic acid, naphthalene-2-sulfonic acid, naphthalene-1,5-disulfonic acid, 2- or 3-phosphoglycerate, glucose-6-phosphate, N-cyclohexylsulfamic acid (with the formation of cyclamates), or with other acid organic compounds, such as ascorbic acid. Pharmaceutically acceptable salts of compounds may also be prepared with a pharmaceutically acceptable cation. Suitable pharmaceutically acceptable cations are well known to those skilled in the art and include alkaline, alkaline earth, ammonium and quaternary ammonium cations. Carbonates or hydrogen carbonates are also possible.

[0051] For oligonucleotides, preferred examples of pharmaceutically acceptable salts include but are not limited to (a) salts formed with cations such as sodium, potassium, ammonium, magnesium, calcium, polyamines such as spermine and spermidine, etc.; (b) acid addition salts formed with inorganic acids, for example hydrochloric acid, hydrobromic acid, sulfuric acid, phosphoric acid, nitric acid and the like; (c) salts formed with organic acids such as, for example, acetic acid, oxalic acid, tartaric acid, succinic acid, maleic acid, fumaric acid, gluconic acid, citric acid, malic acid, ascorbic acid, benzoic acid, tannic acid, palmitic acid, alginic acid, polyglutamic acid, naphthalenesulfonic acid, methanesulfonic acid, p-toluenesulfonic acid, naphthalenedisulfonic acid, polygalacturonic acid, and the like; and (d) salts formed from elemental anions such as chlorine, bromine, and iodine.

[0052] The antisense compounds of the present invention can be utilized for diagnostics, therapeutics, prophylaxis and as research reagents and kits. For therapeutics, an animal, preferably a human, suspected of having a disease or disorder, which can be treated by modulating the expression of GFAT, is treated by administering antisense compounds in accordance with this invention. The compounds of the invention can be utilized in pharmaceutical compositions by adding an effective amount of an antisense compound to a suitable pharmaceutically acceptable diluent or carrier. Use of the antisense compounds

and methods of the invention may also be useful prophylactically, e.g., to prevent or delay infection, inflammation or tumor formation, for example.

[0053] The antisense compounds of the invention are useful for research and diagnostics, because these compounds hybridize to nucleic acids encoding GFAT, enabling sandwich and other assays to easily be constructed to exploit this fact. Hybridization of the antisense oligonucleotides of the invention with a nucleic acid encoding GFAT can be detected by means known in the art. Such means may include conjugation of an enzyme to the oligonucleotide, radiolabelling of the oligonucleotide or any other suitable detection means. Kits using such detection means for detecting the level of GFAT in a sample may also be prepared.

[0054] The present invention also includes pharmaceutical compositions and formulations, which include the antisense compounds of the invention. The pharmaceutical compositions of the present invention may be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration may be topical (including ophthalmic and to mucous membranes including vaginal and rectal delivery), pulmonary, e.g., by inhalation or insufflation of powders or aerosols, including by nebulizer, intratracheal, intranasal, epidermal and transdermal), oral or parenteral. Parenteral administration includes intravenous, intraarterial, subcutaneous, intraperitoneal or intramuscular injection or infusion; or intracranial, e.g., intrathecal or intraventricular, administration. Oligonucleotides with at least one 2'-O-methoxyethyl modification are believed to be particularly useful for oral administration.

[0055] Pharmaceutical compositions and formulations for topical administration may include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids, and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like may be necessary or desirable. Coated condoms, gloves, and the like may also be useful.

[0056] Compositions and formulations for oral administration include powders or granules, suspensions, or solutions in water or non-aqueous media,

capsules, sachets, or tablets. Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids, or binders may be desirable.

[0057] Compositions and formulations for parenteral, intrathecal or intraventricular administration may include sterile aqueous solutions, which may also contain buffers, diluents and other suitable additives such as, but not limited to, penetration enhancers, carrier compounds and other pharmaceutically acceptable carriers or excipients.

[0058] Pharmaceutical compositions of the present invention include, but are not limited to, solutions, emulsions, and liposome-containing formulations. These compositions may be generated from a variety of components that include, but are not limited to, preformed liquids, self-emulsifying solids and self-emulsifying semisolids.

[0059] The pharmaceutical formulations of the present invention, which may conveniently be presented in unit dosage form, may be prepared according to conventional techniques well known in the pharmaceutical industry. Such techniques include the step of bringing into association the active ingredients with the pharmaceutical carrier(s) or excipient(s). In general the formulations are prepared by uniformly and intimately bringing into association the active ingredients with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product.

[0060] The compositions of the present invention may be formulated into any of many possible dosage forms such as, but not limited to, tablets, capsules, liquid syrups, soft gels, suppositories, and enemas. The compositions of the present invention may also be formulated as suspensions in aqueous, non-aqueous or mixed media. Aqueous suspensions may further contain substances, which increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol, and/or dextran. The suspension may also contain stabilizers.

[0061] In one embodiment of the present invention the pharmaceutical compositions may be formulated and used as foams. Pharmaceutical foams include formulations such as, but not limited to, emulsions, microemulsions, creams, jellies, and liposomes. While basically similar in nature these formulations vary in the components and the consistency of the final product.

The preparation of such compositions and formulations is generally known to those skilled in the pharmaceutical and formulation arts and may be applied to the formulation of the compositions of the present invention.

Emulsions

[0062] The compositions of the present invention may be prepared and formulated as emulsions. Emulsions are typically heterogenous systems of one liquid dispersed in another in the form of droplets usually exceeding 0.1 μm in diameter. (Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199; Rosoff, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., Volume 1, p. 245; Block in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 2, p. 335; Higuchi et al., in *Remington's Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA, 1985, p. 301). Emulsions are often biphasic systems comprising of two immiscible liquid phases intimately mixed and dispersed with each other. In general, emulsions may be either water-in-oil (w/o) or of the oil-in-water (o/w) variety. When an aqueous phase is finely divided into and dispersed as minute droplets into a bulk oily phase the resulting composition is called a water-in-oil (w/o) emulsion. Alternatively, when an oily phase is finely divided into and dispersed as minute droplets into a bulk aqueous phase the resulting composition is called an oil-in-water (o/w) emulsion. Emulsions may contain additional components in addition to the dispersed phases and the active drug, which may be present as a solution in either the aqueous phase, oily phase or itself as a separate phase. Pharmaceutical excipients such as emulsifiers, stabilizers, dyes, and anti-oxidants may also be present in emulsions as needed. Pharmaceutical emulsions may also be multiple emulsions that are comprised of more than two phases such as, for example, in the case of oil-in-water-in-oil (o/w/o) and water-in-oil-in-water (w/o/w) emulsions. Such complex formulations often provide certain advantages that simple binary emulsions do not. Multiple emulsions in which individual oil droplets of an o/w emulsion enclose small water droplets

constitute a w/o/w emulsion. Likewise a system of oil droplets enclosed in globules of water stabilized in an oily continuous provides an o/w/o emulsion.

[0063] Emulsions are characterized by little or no thermodynamic stability. Often, the dispersed or discontinuous phase of the emulsion is well dispersed into the external or continuous phase and maintained in this form through the means of emulsifiers or the viscosity of the formulation. Either of the phases of the emulsion may be a semisolid or a solid, as is the case of emulsion-style ointment bases and creams. Other means of stabilizing emulsions entail the use of emulsifiers that may be incorporated into either phase of the emulsion. Emulsifiers may broadly be classified into four categories: synthetic surfactants, naturally occurring emulsifiers, absorption bases, and finely dispersed solids (Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199).

[0064] Synthetic surfactants, also known as surface active agents, have found wide applicability in the formulation of emulsions and have been reviewed in the literature (Rieger, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 285; Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), Marcel Dekker, Inc., New York, N.Y., 1988, volume 1, p. 199). Surfactants are typically amphiphilic and comprise a hydrophilic and a hydrophobic portion. The ratio of the hydrophilic to the hydrophobic nature of the surfactant has been termed the hydrophile/lipophile balance (HLB) and is a valuable tool in categorizing and selecting surfactants in the preparation of formulations. Surfactants may be classified into different classes based on the nature of the hydrophilic group: nonionic, anionic, cationic, and amphoteric (Rieger, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 285).

[0065] Naturally occurring emulsifiers used in emulsion formulations include lanolin, beeswax, phosphatides, lecithin and acacia. Absorption bases possess hydrophilic properties such that they can soak up water to form w/o emulsions yet retain their semisolid consistencies, such as anhydrous lanolin and hydrophilic petrolatum. Finely divided solids have also been used as good emulsifiers especially in combination with surfactants and in viscous

preparations. These include polar inorganic solids, such as heavy metal hydroxides, nonswelling clays such as bentonite, attapulgite, hectorite, kaolin, montmorillonite, colloidal aluminum silicate and colloidal magnesium aluminum silicate, pigments and nonpolar solids such as carbon or glyceryl tristearate.

[0066] A large variety of non-emulsifying materials are also included in emulsion formulations and contribute to the properties of emulsions. These include fats, oils, waxes, fatty acids, fatty alcohols, fatty esters, humectants, hydrophilic colloids, preservatives, and antioxidants (Block, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 335; Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199).

[0067] Hydrophilic colloids or hydrocolloids include naturally occurring gums and synthetic polymers such as polysaccharides (for example, acacia, agar, alginic acid, carrageenan, guar gum, karaya gum, and tragacanth), cellulose derivatives (for example, carboxymethylcellulose and carboxypropylcellulose), and synthetic polymers (for example, carbomers, cellulose ethers, and carboxyvinyl polymers). These disperse or swell in water to form colloidal solutions that stabilize emulsions by forming strong interfacial films around the dispersed phase droplets and by increasing the viscosity of the external phase.

[0068] Since emulsions often contain a number of ingredients such as carbohydrates, proteins, sterols, and phosphatides that may readily support the growth of microbes, these formulations often incorporate preservatives. Commonly used preservatives included in emulsion formulations include methyl paraben, propyl paraben, quaternary ammonium salts, benzalkonium chloride, esters of p-hydroxybenzoic acid, and boric acid. Antioxidants are also commonly added to emulsion formulations to prevent deterioration of the formulation. Antioxidants used may be free radical scavengers such as tocopherols, alkyl gallate, butylated hydroxyanisole, butylated hydroxytoluene, or reducing agents such as ascorbic acid and sodium metabisulfite, and antioxidant synergists such as citric acid, tartaric acid, and lecithin.

[0069] The application of emulsion formulations via dermatological, oral, and parenteral routes and methods for their manufacture have been reviewed in the literature (Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199). Emulsion formulations for oral delivery have been very widely used because of reasons of ease of formulation, efficacy from an absorption and bioavailability standpoint. (Rosoff, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245; Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199). Mineral-oil base laxatives, oil-soluble vitamins, and high fat nutritive preparations are among the materials that have commonly been administered orally as o/w emulsions.

[0070] In one embodiment of the present invention, the compositions of oligonucleotides and nucleic acids are formulated as microemulsions. A microemulsion may be defined as a system of water, oil, and amphiphile, which is a single optically isotropic, and thermodynamically stable liquid solution (Rosoff, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245). Typically microemulsions are systems that are prepared by first dispersing an oil in an aqueous surfactant solution and then adding a sufficient amount of a fourth component, generally an intermediate chain-length alcohol to form a transparent system. Therefore, microemulsions have also been described as thermodynamically stable, isotropically clear dispersions of two immiscible liquids that are stabilized by interfacial films of surface-active molecules (Leung and Shah, in: *Controlled Release of Drugs: Polymers and Aggregate Systems*, Rosoff, M., Ed., 1989, VCH Publishers, New York, pages 1852'5). Microemulsions commonly are prepared via a combination of three to five components that include oil, water, surfactant, cosurfactant, and electrolyte. Whether the microemulsion is of the water-in-oil (w/o) or an oil-in-water (o/w) type is dependent on the properties of the oil and surfactant used and on the structure and geometric packing of the polar heads and hydrocarbon tails of the

surfactant molecules (Schott, in *Remington's Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA, 1985, p. 271).

[0071] The phenomenological approach utilizing phase diagrams has been extensively studied and has yielded a comprehensive knowledge, to one skilled in the art, of how to formulate microemulsions (Rosoff, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245; Block, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 335). Compared to conventional emulsions, microemulsions offer the advantage of solubilizing water-insoluble drugs in a formulation of thermodynamically stable droplets that are formed spontaneously.

[0072] Surfactants used in the preparation of microemulsions include, but are not limited to, ionic surfactants, non-ionic surfactants, Brij 96, polyoxyethylene oleyl ethers, polyglycerol fatty acid esters, tetraglycerol monolaurate (ML310), tetraglycerol monooleate (MO310), hexaglycerol monooleate (PO310), hexaglycerol pentaoleate (PO500), decaglycerol monocaprate (MCA750), decaglycerol monooleate (MO750), decaglycerol sequioleate (S0750), decaglycerol decaoleate (DAO750), alone or in combination with cosurfactants. The cosurfactant, usually a short-chain alcohol such as ethanol, 1-propanol, and 1-butanol, serves to increase the interfacial fluidity by penetrating into the surfactant film and consequently creating a disordered film because of the void space generated among surfactant molecules. Microemulsions may, however, be prepared without the use of cosurfactants and alcohol-free self-emulsifying microemulsion systems are known in the art. The aqueous phase may typically be, but is not limited to, water, an aqueous solution of the drug, glycerol, PEG300, PEG400, polyglycerols, propylene glycols, and derivatives of ethylene glycol. The oil phase may include, but is not limited to, materials such as Captex 300, Captex 355, Capmul MCM, fatty acid esters, medium chain (C8-C12) mono, di, and triglycerides, polyoxyethylated glyceryl fatty acid esters, fatty alcohols, polyglycolized glycerides, saturated polyglycolized C8-C10 glycerides, vegetable oils and silicone oil.

[0073] Microemulsions are particularly of interest from the standpoint of drug solubilization and the enhanced absorption of drugs. Lipid based microemulsions (both o/w and w/o) have been proposed to enhance the oral bioavailability of drugs, including peptides (Constantinides et al., *Pharmaceutical Research*, 1994, 11, 1385-1390; Ritschel, *Meth. Find. Exp. Clin. Pharmacol.,* 1993, 13, 205). Microemulsions afford advantages of improved drug solubilization, protection of drug from enzymatic hydrolysis, possible enhancement of drug absorption due to surfactant-induced alterations in membrane fluidity and permeability, ease of preparation, ease of oral administration over solid dosage forms, improved clinical potency, and decreased toxicity (Constantinides et al., *Pharmaceutical Research*, 1994, 11, 1385; Ho et al., *J. Pharm. Sci.*, 1996, 85, 138-143). Often microemulsions may form spontaneously when their components are brought together at ambient temperature. This may be particularly advantageous when formulating thermolabile drugs, peptides, or oligonucleotides. Microemulsions have also been effective in the transdermal delivery of active components in both cosmetic and pharmaceutical applications. It is expected that the microemulsion compositions and formulations of the present invention will facilitate the increased systemic absorption of oligonucleotides and nucleic acids from the gastrointestinal tract, as well as improve the local cellular uptake of oligonucleotides and nucleic acids within the gastrointestinal tract, vagina, buccal cavity and other areas of administration.

[0074] Microemulsions of the present invention may also contain additional components and additives such as sorbitan monostearate (Grill 3), Labrasol, and penetration enhancers to improve the properties of the formulation and to enhance the absorption of the oligonucleotides and nucleic acids of the present invention. Penetration enhancers used in the microemulsions of the present invention may be classified as belonging to one of five broad categories - surfactants, fatty acids, bile salts, chelating agents, and non-chelating non-surfactants (Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, p. 92). Each of these classes has been discussed above.

Liposomes

[0075] There are many organized surfactant structures besides microemulsions that have been studied and used for the formulation of drugs. These include monolayers, micelles, bilayers, and vesicles. Vesicles, such as liposomes, have attracted great interest because of their specificity and the duration of action they offer from the standpoint of drug delivery. As used in the present invention, the term "liposome" means a vesicle composed of amphiphilic lipids arranged in a spherical bilayer or bilayers.

[0076] Liposomes are unilamellar or multilamellar vesicles which have a membrane formed from a lipophilic material and an aqueous interior. The aqueous portion contains the composition to be delivered. Cationic liposomes possess the advantage of being able to fuse to the cell wall. Noncationic liposomes, although not able to fuse as efficiently with the cell wall, are taken up by macrophages in vivo.

[0077] In order to cross intact mammalian skin, lipid vesicles must pass through a series of fine pores, each with a diameter less than 50 nm, under the influence of a suitable transdermal gradient. Therefore, it is desirable to use a liposome, which is highly deformable and able to pass through such fine pores.

[0078] Further advantages of liposomes include; liposomes obtained from natural phospholipids are biocompatible and biodegradable; liposomes can incorporate a wide range of water and lipid soluble drugs; liposomes can protect encapsulated drugs in their internal compartments from metabolism and degradation (Rosoff, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, P. 245). Important considerations in the preparation of liposome formulations are the lipid surface charge, vesicle size, and the aqueous volume of the liposomes.

[0079] Liposomes are useful for the transfer and delivery of active ingredients to the site of action. Because the liposomal membrane is structurally similar to biological membranes, when liposomes are applied to a tissue, the liposomes start to merge with the cellular membranes. As the merging of the liposome and cell progresses, the liposomal contents are emptied into the cell where the active agent may act.

[0080] Liposomal formulations have been the focus of extensive investigation as the mode of delivery for many drugs. There is growing evidence that for topical administration, liposomes present several advantages over other formulations. Such advantages include reduced side-effects related to high systemic absorption of the administered drug, increased accumulation of the administered drug at the desired target, and the ability to administer a wide variety of drugs, both hydrophilic and hydrophobic, into the skin.

[0081] Several reports have detailed the ability of liposomes to deliver agents including high-molecular weight DNA into the skin. Compounds including analgesics, antibodies, hormones, and high-molecular weight DNAs have been administered to the skin. The majority of applications resulted in the targeting of the upper epidermis.

[0082] Liposomes fall into two broad classes. Cationic liposomes are positively charged liposomes, which interact with the negatively charged DNA molecules to form a stable complex. The positively charged DNA/liposome complex binds to the negatively charged cell surface and is internalized in an endosome. Due to the acidic pH within the endosome, the liposomes are ruptured, releasing their contents into the cell cytoplasm (Wang et al., *Biochem. Biophys. Res. Commun.*, 1987, 147, 980 - 985).

[0083] Liposomes, which are pH-sensitive or negatively charged, entrap DNA rather than complex with it. Since both the DNA and the lipid are similarly charged, repulsion rather than complex formation occurs. Nevertheless, some DNA is entrapped within the aqueous interior of these liposomes. pH-sensitive liposomes have been used to deliver DNA encoding the thymidine kinase gene to cell monolayers in culture. Expression of the exogenous gene was detected in the target cells (Zhou et al., *Journal of Controlled Release*, 1992, 19, 269-274).

[0084] One major type of liposomal composition includes phospholipids other than naturally derived phosphatidylcholine. Neutral liposome compositions, for example, can be formed from dimyristoyl phosphatidylcholine (DMPC) or dipalmitoyl phosphatidylcholine (DPPC). Anionic liposome compositions generally are formed from dimyristoyl phosphatidylglycerol, while anionic fusogenic liposomes are formed primarily

from dioleoyl phosphatidylethanolamine (DOPE). Another type of liposomal composition is formed from phosphatidylcholine (PC) such as, for example, soybean PC, and egg PC. Another type is formed from mixtures of phospholipid and/or phosphatidylcholine and/or cholesterol.

[0085] Several studies have assessed the topical delivery of liposomal drug formulations to the skin. Application of liposomes containing interferon to guinea pig skin resulted in a reduction of skin herpes sores while delivery of interferon via other means (e.g. as a solution or as an emulsion) were ineffective (Weiner et al., *Journal of Drug Targeting*, 1992, 2, 405-410). Further, an additional study tested the efficacy of interferon administered as part of a liposomal formulation to the administration of interferon using an aqueous system, and concluded that the liposomal formulation was superior to aqueous administration (du Plessis et al., *Antiviral Research*, 1992, 18, 259-265).

[0086] Non-ionic liposomal systems have also been examined to determine their utility in the delivery of drugs to the skin, in particular systems comprising non-ionic surfactant and cholesterol. Non-ionic liposomal formulations comprising Novasome ™ I (glyceryl dilaurate/cholesterol/polyoxyethylene-10-stearyl ether) and Novasome™ II (glyceryl distearate/ cholesterol/polyoxyethylene-10-stearyl ether) were used to deliver cyclosporin-A into the dermis of mouse skin. Results indicated that such non-ionic liposomal systems were effective in facilitating the deposition of cyclosporin-A into different layers of the skin (Hu et al. *S.T.P.Pharma. Sci.*, 1994, 4, 6, 466).

[0087] Liposomes also include "sterically stabilized" liposomes, a term which, as used herein, refers to liposomes comprising one or more specialized lipids that, when incorporated into liposomes, result in enhanced circulation lifetimes relative to liposomes lacking such specialized lipids. Examples of sterically stabilized liposomes are those in which part of the vesicle-forming lipid portion of the liposome (A) comprises one or more glycolipids, such as monosialoganglioside GM1, or (B) is derivatized with one or more hydrophilic polymers, such as a polyethylene glycol (PEG) moiety. While not wishing to be bound by any particular theory, it is thought in the art that, at least for sterically stabilized liposomes containing gangliosides, sphingomyelin, or PEG-derivatized lipids, the enhanced circulation half-life of these sterically stabilized

liposomes derives from a reduced uptake into cells of the reticuloendothelial system (RES) (Allen et al., *FEBS Letters*, 1987, 223, 42; Wu et al., *Cancer Research*, 1993, 53, 3765).

[0088] Various liposomes comprising one or more glycolipids are known in the art. Papahadjopoulos et al. (*Ann. N.Y. Acad. Sci.*, 1987, 507, 64) reported the ability of monosialoganglioside GM1, galactocerebroside sulfate, and phosphatidylinositol to improve blood half-lives of liposomes. These findings were expounded upon by Gabizon et al. (*Proc. Natl. Acad. Sci. U.S.A.*, 1988, 85, 6949), U.S. Patent No. 4,837,028 and WO 88/04924, both to Allen et al., disclose liposomes comprising (1) sphingomyelin and (2) the ganglioside Gjor a galactocerebroside sulfate ester. U.S. Patent No. 5,543,152 (Webb et al.) discloses liposomes comprising sphingomyelin. Liposomes comprising 1,2-sn-dimyristoylphosphatidylcholine are disclosed in WO 97/13499 (Lim et al.).

[0089] Many liposomes comprising lipids derivatized with one or more hydrophilic polymers, and methods of preparation thereof, are known in the art. Sunamoto et al. (*Bull. Chem. Soc. Jpn.*, 1980, 53, 2778) described liposomes comprising a nonionic detergent, 2C1215G, which contains a PEG moiety. Illum et al. (*FEBS Lett.*, 1984, 167, 79) noted that hydrophilic coating of polystyrene particles with polymeric glycols results in significantly enhanced blood half-lives. Synthetic phospholipids modified by the attachment of carboxylic groups of polyalkylene glycols (e.g., PEG) are described by Sears (U.S. Patent Nos. 4,426,330 and 4,534,899). Klibanov et al. (*FEBS Lett.*, 1990, 268, 235) described experiments demonstrating that liposomes comprising phosphatidylethanolamine (PE) derivatized with PEG or PEG stearate have significant increases in blood circulation half-lives. Blume et al. (*Biochimica et Biophysica Acta*, 1990, 1029, 91) extended such observations to other PEG derivatized phospholipids, e.g., DSPE-PEG, formed from the combination of distearoylphosphatidylethanolamine (DSPE) and PEG. Liposomes having covalently bound PEG moieties on their external surface are described in European Patent No. EP 0 445 131 B1 and WO 90/04384 to Fisher. Liposome compositions containing 1-20 mole percent of PE derivatized with PEG, and methods of use thereof, are described by Woodle et al. (U.S. Patent Nos. 5,013,556 and 5,356,633) and Martin et al. (U.S. Patent No. 5,213,804 and

European Patent No. EP 0 496 813 Bl). Liposomes comprising a number of other lipid-polymer conjugates are disclosed in WO 91/05545 and U.S. Patent No. 5,225,212 (both to Martin et al.) and in WO 94/20073 (Zalipsky et al.) Liposomes comprising PEG-modified ceramide lipids are described in WO 96/10391 (Choi et al.). U.S. Patent Nos. 5,540,935 (Miyazaki et al.) and 5,556,948 (Tagawa et al.) describe PEG-containing liposomes that can be further derivatized with functional moieties on their surfaces.

[0090] A limited number of liposomes comprising nucleic acids are known in the art. WO 96/40062 to Thierry et al. discloses methods for encapsulating high molecular weight nucleic acids in liposomes. U.S. Patent No. 5,264,221 to Tagawa et al. discloses protein-bonded liposomes and asserts that the contents of such liposomes may include an antisense RNA. U.S. Patent No. 5,665,710 to Rahman et al. describes certain methods of encapsulating oligodeoxynucleotides in liposomes. WO 97/04787 to Love et al. discloses liposomes comprising antisense oligonucleotides targeted to the raf gene.

[0091] Transfersomes are yet another type of liposomes, and are highly deformable lipid aggregates which are attractive candidates for drug delivery vehicles. Transfersomes may be described as lipid droplets that are so highly deformable that they are easily able to penetrate through pores that are smaller than the droplet. Transfersomes are adaptable to the environment in which they are used, e.g. they are self-optimizing (adaptive to the shape of pores in the skin), self-repairing, frequently reach their targets without fragmenting, and often self-loading. To make transfersomes it is possible to add surface edge-activators, usually surfactants, to a standard liposomal composition. Transfersomes have been used to deliver serum albumin to the skin. The transfersome-mediated delivery of serum albumin has been shown to be as effective as subcutaneous injection of a solution containing serum albumin.

[0092] Surfactants find wide application in formulations such as emulsions (including microemulsions) and liposomes. The most common way of classifying and ranking the properties of the many different types of surfactants, both natural and synthetic, is by the use of the hydrophile/lipophile balance (HLB). The nature of the hydrophilic group (also known as the "head") provides the most useful means for categorizing the different surfactants used in

formulations (Rieger, in *Pharmaceutical Dosage Forms*, Marcel Dekker, Inc., New York, NY, 1988, p. 285).

[0093] If the surfactant molecule is not ionized, it is classified as a nonionic surfactant. Nonionic surfactants find wide application in pharmaceutical and cosmetic products and are usable over a wide range of pH values. In general their HLB values range from 2 to about 18 depending on their structure. Nonionic surfactants include nonionic esters such as ethylene glycol esters, propylene glycol esters, glyceryl esters, polyglyceryl esters, sorbitan esters, sucrose esters, and ethoxylated esters. Nonionic alkanolamides and ethers such as fatty alcohol ethoxylates, propoxylated alcohols, and ethoxylated/propoxylated block polymers are also included in this class. The polyoxyethylene surfactants are the most popular members of the nonionic surfactant class.

[0094] If the surfactant molecule carries a negative charge when it is dissolved or dispersed in water, the surfactant is classified as anionic. Anionic surfactants include carboxylates such as soaps, acyl lactylates, acyl amides of amino acids, esters of sulfuric acid such as alkyl sulfates and ethoxylated alkyl sulfates, sulfonates such as alkyl benzene sulfonates, acyl isethionates, acyl taurates and sulfosuccinates, and phosphates. The most important members of the anionic surfactant class are the alkyl sulfates and the soaps.

[0095] If the surfactant molecule carries a positive charge when it is dissolved or dispersed in water, the surfactant is classified as cationic. Cationic surfactants include quaternary ammonium salts and ethoxylated amines. The quaternary ammonium salts are the most used members of this class.

[0096] If the surfactant molecule has the ability to carry either a positive or negative charge, the surfactant is classified as amphoteric. Amphoteric surfactants include acrylic acid derivatives, substituted alkylamides, N-alkylbetaines, and phosphatides.

[0097] The use of surfactants in drug products, formulations and in emulsions has been reviewed (Rieger, in *Pharmaceutical Dosage Forms*, Marcel Dekker, Inc., New York, NY, 1988, p. 285).

Penetration Enhancers

[0098] In one embodiment, the present invention employs various penetration enhancers to effect the efficient delivery of nucleic acids particularly oligonucleotides, to the skin of animals. Most drugs are present in solution in both ionized and nonionized forms. However, usually only lipid soluble or lipophilic drugs readily cross cell membranes. It has been discovered that even non-lipophilic drugs may cross cell membranes if the membrane to be crossed is treated with a penetration enhancer. In addition to aiding the diffusion of non-lipophilic drugs across cell membranes, penetration enhancers also enhance the permeability of lipophilic drugs.

[0099] Penetration enhancers may be classified as belonging to one of five broad categories, i.e., surfactants, fatty acids, bile salts, chelating agents, and non-chelating nonsurfactants (Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, p.92). Each of the above mentioned classes of penetration enhancers are described below in greater detail.

[00100] Surfactants: In connection with the present invention, surfactants (or "surface-active agents") are chemical entities which, when dissolved in an aqueous solution, reduce the surface tension of the solution or the interfacial tension between the aqueous solution and another liquid, with the result that absorption of oligonucleotides through the mucosa is enhanced. In addition to bile salts and fatty acids, these penetration enhancers include, for example, sodium lauryl sulfate, polyoxyethylene-9-lauryl ether and polyoxyethylene-20-cetyl ether) (Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, p.92); and perfluorochemical emulsions, such as FC-43. Takahashi et al., *J. Pharm. Pharmacol.*, 1988, 40, 252).

[00101] Fatty acids: Various fatty acids and their derivatives which act as penetration enhancers include, for example, oleic acid, lauric acid, capric acid (n-decanoic acid), myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein (1-monooleoyl-.rac-glycerol), dilaurin, caprylic acid, arachidonic acid, glycerol 1-monocaprate, 1-dodecylazacycloheptan-2-one, acylcarnitines, acylcholines, C1-10 alkyl esters thereof (e.g., methyl, isopropyl and t-butyl), and mono- and di-glycerides thereof (i.e., oleate, laurate, caprate, myristate, palmitate, stearate, linoleate, etc.) (Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991,

p.92; Muranishi, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1990, 7, 1-33; El Hariri et al., *J. Pharm. Pharmacol.*, 1992, 44, 651-654).

[00102] Bile salts: The physiological role of bile includes the facilitation of dispersion and absorption of lipids and fat-soluble vitamins (Brunton, Chapter 38 in: Goodman & Gilman's *The Pharmacological Basis of Therapeutics*, 9th Ed., Hardman et al. Eds. McGraw-Hill, New York, 1996, pp. 934-935). Various natural bile salts, and their synthetic derivatives, act as penetration enhancers. Thus the term "bile salts" includes any of the naturally occurring components of bile as well as any of their synthetic derivatives. The bile salts of the invention include, for example, cholic acid (or its pharmaceutically acceptable sodium salt, sodium cholate), dehydrocholic acid (sodium dehydrocholate), deoxycholic acid (sodium deoxycholate), glucholic acid (sodium glucholate), glycholic acid (sodium glycocholate), glycodeoxycholic acid (sodium glycodeoxycholate), taurocholic acid (sodium taurocholate), taurodeoxycholic acid (sodium taurodeoxycholate), chenodeoxycholic acid (sodium chenodeoxycholate), ursodeoxycholic acid (UDCA), sodium tauro-24,25-dihydro-fusidate (STDHF), sodium glycodihydrofusidate and polyoxyethylene-9-lauryl ether (POE) (Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, page 92; Swinyard, Chapter 39 In: *Remington's Pharmaceutical Sciences*, 18th Ed., Gennaro, ed., Mack Publishing Co., Easton, PA, 1990, pages 782-783; Muranishi, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1990, 7, 1-33; Yamamoto et al., *J. Pharm. Exp. Ther.*, 1992, 263, 25; Yamashita et al., *J. Pharm. Sci.*, 1990, 79, 579-583).

[00103] Chelating Agents: Chelating agents, as used in connection with the present invention, can be defined as compounds that remove metallic ions from solution by forming complexes therewith, with the result that absorption of oligonucleotides through the mucosa is enhanced. With regards to their use as penetration enhancers in the present invention, chelating agents have the added advantage of also serving as DNase inhibitors, as most characterized DNA nucleases require a divalent metal ion for catalysis and are thus inhibited by chelating agents (Jarrett, *J. Chromatogr.*, 1993, 618, 315-339). Chelating agents of the invention include but are not limited to disodium ethylenediaminetetraacetate (EDTA), citric acid, salicylates (e.g., sodium

salicylate, 5-methoxysalicylate and homovanilate), N-acyl derivatives of collagen, laureth-9 and N-amino acyl derivatives of beta-diketones (enamines)(Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, page 92; Muranishi, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1990, 7, 1-33; Buur et al., *J. Control Rel.*, 1990, 14, 43-51).

[00104] Non-chelating non-surfactants: As used herein, nonchelating non-surfactant penetration enhancing compounds can be defined as compounds that demonstrate insignificant activity as chelating agents or as surfactants but that nonetheless enhance absorption of oligonucleotides through the alimentary mucosa (Muranishi, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1990, 7, 1-33). This class of penetration enhancers includes, for example, unsaturated cyclic ureas, 1-alkyl- and 1-alkenylazacyclo-alkanone derivatives (Lee et al., *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, page 92); and non-steroidal anti-inflammatory agents such as diclofenac sodium, indomethacin, and phenylbutazone (Yamashita et al., *J. Pharm. Pharmacol.*, 1987, 39, 621-626).

[00105] Agents that enhance uptake of oligonucleotides at the cellular level may also be added to the pharmaceutical and other compositions of the present invention. For example, cationic lipids, such as lipofectin (Junichi et al, U.S. Patent No. 5,705,188), cationic glycerol derivatives, and polycationic molecules, such as polylysine (Lollo et al., PCT Application WO 97/30731), are also known to enhance the cellular uptake of oligonucleotides.

[00106] Other agents may be utilized to enhance the penetration of the administered nucleic acids, including glycols such as ethylene glycol and propylene glycol, pyrrols such as 2-pyrrol, azones, and terpenes such as limonene and menthone.

Carriers

[00107] Certain compositions of the present invention also incorporate carrier compounds in the formulation. As used herein, "carrier compound" or "carrier" can refer to a nucleic acid, or analog thereof, which is inert (i.e., does not possess biological activity per se) but is recognized as a nucleic acid by in vivo processes that reduce the bioavailability of a nucleic acid having biological

activity by, for example, degrading the biologically active nucleic acid or promoting its removal from circulation. The coadministration of a nucleic acid and a carrier compound, typically with an excess of the latter substance, can result in a substantial reduction of the amount of nucleic acid recovered in the liver, kidney or other extracirculatory reservoirs, presumably due to competition between the carrier compound and the nucleic acid for a common receptor. For example, the recovery of a partially phosphorothioate oligonucleotide in hepatic tissue can be reduced when it is coadministered with polyinosinic acid, dextran sulfate, polycytidic acid or 4-acetamido-4'isothiocyano-stilbene-2,2'disulfonic acid (Miyao et al., *Antisense Res. Dev.*, 1995, 5, 115-121; Takakura et al., *Antisense & Nucl. Acid Drug Dev.*, 1996, 6, 177-183).

Excipients

[00108] In contrast to a carrier compound, a "pharmaceutical carrier" or "excipient" is a pharmaceutically acceptable solvent, suspending agent or any other pharmacologically inert vehicle for delivering one or more nucleic acids to an animal. The excipient may be liquid or solid and is selected, with the planned manner of administration in mind, so as to provide for the desired bulk, consistency, etc., when combined with a nucleic acid and the other components of a given pharmaceutical composition. Typical pharmaceutical carriers include, but are not limited to, binding agents (e.g., pregelatinized maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose, etc.); fillers (e.g., lactose and other sugars, microcrystalline cellulose, pectin, gelatin, calcium sulfate, ethyl cellulose, polyacrylates or calcium hydrogen phosphate, etc.); lubricants (e.g., magnesium stearate, talc, silica, colloidal silicon dioxide, stearic acid, metallic stearates, hydrogenated vegetable oils, corn starch, polyethylene glycols, sodium benzoate, sodium acetate, etc.); disintegrants (e.g., starch, sodium starch glycolate, etc.); and wetting agents (e.g., sodium lauryl sulphate, etc.).

[00109] Pharmaceutically acceptable organic or inorganic excipient suitable for non-parenteral administration, which does not deleteriously react with nucleic acids, can also be used to formulate the compositions of the present invention. Suitable pharmaceutically acceptable carriers include, but are not limited to, water, salt solutions, alcohols, polyethylene glycols, gelatin, lactose,

amylose, magnesium stearate, talc, silicic acid, viscous paraffin, hydroxymethylcellulose, polyvinylpyrrolidone and the like.

[00110] Formulations for topical administration of nucleic acids may include sterile and non-sterile aqueous solutions, non-aqueous solutions in common solvents such as alcohols, or solutions of the nucleic acids in liquid or solid oil bases. The solutions may also contain buffers, diluents, and other suitable additives. Pharmaceutically acceptable organic or inorganic excipients suitable for non-parenteral administration that do not deleteriously react with nucleic acids can be used.

[00111] Suitable pharmaceutically acceptable excipients include, but are not limited to, water, salt solutions, alcohol, polyethylene glycols, gelatin, lactose, amylose, magnesium stearate, talc, silicic acid, viscous paraffin, hydroxymethylcellulose, polyvinylpyrrolidone and the like.

Other Components

[00112] The compositions of the present invention may additionally contain other adjunct components conventionally found in pharmaceutical compositions, at their art-established usage levels. Thus, for example, the compositions may contain additional, compatible, pharmaceutically-active materials such as, for example, antipruritics, astringents, local anesthetics or anti-inflammatory agents, or may contain additional materials useful in physically formulating various dosage forms of the compositions of the present invention, such as dyes, flavoring agents, preservatives, antioxidants, opacifiers, thickening agents and stabilizers. However, such materials, when added, should not unduly interfere with the biological activities of the components of the compositions of the present invention.' The formulations can be sterilized and, if desired, mixed with auxiliary agents, e.g., lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, colorings, flavorings and/or aromatic substances and the like which do not deleteriously interact with the nucleic acid(s) of the formulation.

[00113] Aqueous suspensions may contain substances that increase the viscosity of the suspension including, for example, sodium

carboxymethylcellulose, sorbitol, and/or dextran. The suspension may also contain stabilizers.

[00114] Certain embodiments of the invention provide pharmaceutical compositions containing (a) one or more antisense compounds and (b) one or more other chemotherapeutic agents which function by a non-antisense mechanism. Examples of such chemotherapeutic agents include, but are not limited to, anticancer drugs such as daunorubicin, dactinomycin, doxorubicin, bleomycin, mitomycin, nitrogen mustard, chlorambucil, melphalan, cyclophosphamide, 6-mercaptopurine, 6-thioguanine, cytarabine (CA), 5-fluorouracil (5-FU), floxuridine (5-FUdR), methotrexate (MTX), colchicine, vincristine, vinblastine, etoposide, teniposide, cisplatin and diethylstilbestrol (DES). See, generally, *The Merck Manual of Diagnosis and Therapy*, 15th Ed., Berkow et al., eds., 1987, Rahway, N.J., pages 1206-1228). Anti-inflammatory drugs, including but not limited to nonsteroidal anti-inflammatory drugs and corticosteroids, and antiviral drugs, including but not limited to ribivirin, vidarabine, acyclovir and ganciclovir, may also be combined in compositions of the invention. See, generally, *The Merck Manual of Diagnosis and Therapy*, 15th Ed., Berkow et al., eds., 1987, Rahway, N.J., pages 2499-2506 and 46-49, respectively) other non-antisense chemotherapeutic agents are also within the scope of this invention. Two or more combined compounds may be used together or sequentially.

[00115] In another related embodiment, compositions of the invention may contain one or more antisense compounds, particularly oligonucleotides, targeted to a first nucleic acid and one or more additional antisense compounds targeted to a second nucleic acid target. Numerous examples of antisense compounds are known in the art. Two or more combined compounds may be used together or sequentially.

[00116] The formulation of therapeutic compositions and their subsequent administration is believed to be within the skill of those in the art. Dosing is dependent on severity and responsiveness of the disease state to be treated, with the course of treatment lasting from several days to several months, or until a cure is effected or a diminution of the disease state is achieved. Optimal dosing schedules can be calculated from measurements of drug accumulation in the

body of the patient. Persons of ordinary skill can easily determine optimum dosages, dosing methodologies and repetition rates. Optimum dosages may vary depending on the relative potency of individual oligonucleotides, and can generally be estimated based on EC50s found to be effective in in vitro and in vivo animal models. In general, dosage is from 0.01 μg to 100 g per kg of body weight, and may be given once or more daily, weekly, monthly or yearly, or even once every 2 to 20 years. Persons of ordinary skill in the art can easily estimate repetition rates for dosing based on measured residence times and concentrations of the drug in bodily fluids or tissues. Following successful treatment, it may be desirable to have the patient undergo maintenance therapy to prevent the recurrence of the disease state, wherein the oligonucleotide is administered in maintenance doses, ranging from 0.01 μg to 100 g per kg of body weight, once or more daily, to once every 20 years.

[00117] While the present invention has been described with specificity in accordance with certain of its preferred embodiments, the following examples serve only to illustrate the invention and are not intended to limit the same.

EXAMPLES

Example 1

Nucleoside Phosphoramidites for Oligonucleotide Synthesis Deoxy and 2'-alkoxy amidites

[00118] 2'-Deoxy and 2'-methoxy beta-cyanoethyldiisopropyl phosphoramidites are available from commercial sources (e.g. Chemgenes, Needham MA or Glen Research, Inc. Sterling VA). Other 2'-O-alkoxy substituted nucleoside amidites are prepared as described in U.S. Patent 5,506,351, herein incorporated by reference. For oligonucleotides synthesized using 2'-alkoxy amidites, the standard cycle for unmodified oligonucleotides is utilized, except the wait step after pulse delivery of tetrazole and base is increased to 360 seconds.

[00119] Oligonucleotides containing 5-methyl-2'-deoxycytidine (5-Me-C) nucleotides are synthesized according to published methods [Sanghvi, et. al.,

Nucleic Acids Research, 1993, 21, 3197-3203] using commercially available phosphoramidites (Glen Research, Sterling VA or ChemGenes, Needham MA).

2'-Fluoro amidites

2'-Fluorodeoxyadenosine amidites

[00120] 2'-fluoro oligonucleotides are synthesized as described previously [Kawasaki, et. al., *J. Med. Chem.*, 1993, 36, 831-841] and United States patent 5,670,633, herein incorporated by reference. Briefly, the protected nucleoside N6-benzoyl-2'-deoxy-2'-fluoroadenosine is synthesized utilizing commercially available 9-beta-D-arabinofuranosyladenine as starting material and by modifying literature procedures whereby the 2'-alpha-fluoro atom is introduced by a S_N2-displacement of a 2'-beta-trityl group. Thus N6-benzoyl-9-beta-D-arabinofuranosyladenine is selectively protected in moderate yield as the 3',5'-ditetrahydropyranyl (THP) intermediate. Deprotection of the THP and N6-benzoyl groups is accomplished using standard methodologies and standard methods are used to obtain the 5'-dimethoxytrityl-(DMT) and 5'-DMT-3'-phosphoramidite intermediates.

2'-Fluorodeoxyguanosine

[00121] The synthesis of 2'-deoxy-2'-fluoroguanosine is accomplished using tetraisopropyldisiloxanyl (TPDS) protected 9-beta-D-arabinofuranosylguanine as starting material, and conversion to the intermediate diisobutyrylarabinofuranosylguanosine. Deprotection of the TPDS group is followed by protection of the hydroxyl group with THP to give diisobutyryl di-THP protected arabinofuranosylguanine. Selective O-deacylation and triflation is followed by treatment of the crude product with fluoride, then deprotection of the THP groups. Standard methodologies are used to obtain the 5'-DMT- and 5'-DMT-3'-phosphoramidites.

2'-Fluorouridine

[00122] Synthesis of 2'-deoxy-2'-fluorouridine is accomplished by the modification of a literature procedure in which 2,2'anhydro-1-beta-D-

arabinofuranosyluracil is treated with 70% hydrogen fluoride-pyridine. Standard procedures are used to obtain the 5'-DMT and 5'-DMT-3'-phosphoramidites.

2'-Fluorodeoxycytidine

[00123] 2'-deoxy-2'-fluorocytidine is synthesized via amination of 2'-deoxy-2'-fluorouridine, followed by selective protection to give N4-benzoyl-2'-deoxy-2'-fluorocytidine. Standard procedures are used to obtain the 5'-DMT and 5'-DMT-3'phosphoramidites.

2'-O-(2-Methoxyethyl) modified amidites

[00124] 2'-O-Methoxyethyl-substituted nucleoside amidites are prepared as follows, or alternatively, as per the methods of Martin, P., *Helvetica Chimica Acta*, 1995, 78, 486-504.

2,2'-Anhydro[l-(beta-D-arabinofuranosyl)-5-methyluridinel

[00125] 5-Methyluridine (ribosylthymine, commercially available through Yamasa, Choshi, Japan) (72.0 g, 0.279 M), diphenylcarbonate (90.0 g, 0.420 M) and sodium bicarbonate (2.0 g, 0.024 M) are added to DMF (300 mL). The mixture is heated to reflux, with stirring, allowing the evolved carbon dioxide gas to be released in a controlled manner. After 1 hour, the slightly darkened solution is concentrated under reduced pressure. The resulting syrup is poured into diethylether (2.5 L), with stirring. The product formed a gum. The ether is decanted and the residue is dissolved in a minimum amount of methanol (ca. 400 mL). The solution is poured into fresh ether (2.5 L) to yield a stiff gum. The ether is decanted and the gum is dried in a vacuum oven (60°C at 1 mm Hg for 24 h) to give a solid that is crushed to a light tan powder. The material is used as is for further reactions (or it can be purified further by column chromatography using a gradient of methanol in ethyl acetate (10-25%) to give a white solid.

2'-O-Methoxyethyl-5-methyluridine

[00126] 2,2'-Anhydro-5-methyluridine (195 g, 0.81 M), tris(2-methoxyethyl)borate (231 g, 0.98 M) and 2-methoxyethanol (1.2 L) are added

to a 2 L stainless steel pressure vessel and placed in a pre-heated oil bath at 160°C. After heating for 48 hours at 155-160°C, the vessel is opened and the solution evaporated to dryness and triturated with MeOH (200 mL). The residue is suspended in hot acetone (1 L). The insoluble salts are filtered, washed with acetone (150 mL) and the filtrate evaporated. The residue (280 g) is dissolved in CH_3CN (600 mL) and evaporated. A silica gel column (3 kg) is packed in CH_2Cl_2 /acetone /MeOH (20:5:3) containing 0.5% Et_3NH. The residue is dissolved in CH_2C1_2 (250 mL) and adsorbed onto silica (150 g) prior to loading onto the column. The product is eluted with the packing solvent to give the title product. Additional material can be obtained by reworking impure fractions.

2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine

[00127] 2'-O-Methoxyethyl-5-methyluridine (160 g, 0.506 M) is co-evaporated with pyridine (250 mL) and the dried residue dissolved in pyridine (1.3 L). A first aliquot of dimethoxytrityl chloride (94.3 g, 0.278 M) is added and the mixture stirred at room temperature for one hour. A second aliquot of dimethoxytrityl chloride (94.3 g, 0.278 M) is added and the reaction stirred for an additional one hour. Methanol (170 mL) is then added to stop the reaction. The solvent is evaporated and triturated with CH_3CN (200 mL) The residue is dissolved in CHCl (1.5 L) and extracted with 2x500 mL of saturated $NaHCO_3$ and 2x500 mL of saturated NaCl. The organic phase is dried over Na_2SO_4, filtered, and evaporated. The residue is purified on a 3.5 kg silica gel column, packed and eluted with EtOAc/hexane/ acetone (5:5:1) containing 0-5% Et_3NH. The pure fractions are evaporated to give the title product.

3'-O-Acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine

[00128] 2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine (106 g, 0.167 M), DMF/pyridine (750 mL of a 3:1 mixture prepared from 562 mL of DMF and 188 mL of pyridine) and acetic anhydride (24.38 mL, 0.258 M) are combined and stirred at room temperature for 24 hours. The reaction is monitored by TLC by first quenching the TLC sample with the addition of MeOH. Upon completion of the reaction, as judged by TLC, MeOH (50 mL) is added and the mixture evaporated at 35°C. The residue is dissolved in $CHC1_3$

(800 mL) and extracted with 2x200 mL of saturated sodium bicarbonate and 2x200 mL of saturated NaCl. The water layers are back extracted with 200 mL of $CHCl_3$. The combined organics are dried with sodium sulfate and evaporated to a residue. The residue is purified on a 3.5 kg silica gel column and eluted using EtOAc/hexane(4:1). Pure product fractions are evaporated to yield the title compounds.

3'-O-Acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyl-4-triazoleuridine

[00129] A first solution is prepared by dissolving 3'-O-acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyluridine (96 g, 0.144 M) in CH_3CN (700 mL) and set aside. Triethylamine (189 mL, 1.44 M) is added to a solution of triazole (90 g, 1.3 M) in CH_3CN (1 L), cooled to –5°C and stirred for 0.5 h using an overhead stirrer. $POCl_3$ is added dropwise, over a 30 minute period, to the stirred solution maintained at 0-10°C, and the resulting mixture stirred for an additional 2 hours. The first solution is added dropwise, over a 45 minute period, to the latter solution. The resulting reaction mixture is stored overnight in a cold room. Salts are filtered from the reaction mixture and the solution is evaporated. The residue is dissolved in EtOAc (1 L) and the insoluble solids are removed by filtration. The filtrate is washed with 1x300 mL of $NaHCO_3$ and 2x300 mL of saturated NaCl, dried over sodium sulfate and evaporated. The residue is triturated with EtOAc to give the title compound.

2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine

[00130] A solution of 3'-O-acetyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methyl-4-triazoleuridine (103 g, 0.141 M) in dioxane (500 mL) and NH_4OH (30 mL) is stirred at room temperature for 2 hours. The dioxane solution is evaporated and the residue azeotroped with MeOH (2x200 mL). The residue is dissolved in MeOH (300 mL) and transferred to a 2-liter stainless steel pressure vessel. MeOH (400 mL) saturated with NH_3 gas is added and the vessel heated to 100°C for 2 hours (TLC showed complete conversion). The vessel contents are evaporated to dryness and the residue is dissolved in EtOAc (500 mL) and washed once with saturated NaCl (200 mL). The organics

are dried over sodium sulfate and the solvent is evaporated to give the title compound.

N4-Benzoyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine

[00131] 2'-O-Methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine (85 g, 0.134 M) is dissolved in DMF (800 mL) and benzoic anhydride (37.2 g, 0.165 M) is added with stirring. After stirring for 3 hours, TLC showed the reaction to be approximately 95% complete. The solvent is evaporated and the residue azeotroped with MeOH (200 mL). The residue is dissolved in $CHCl_3$ (700 mL) and extracted with saturated NaHCO, (2x300 mL) and saturated NaCl (2x300 mL), dried over $MgSO_4$ and evaporated to give a residue. The residue is chromatographed on a 1.5 kg silica column using EtOAc/hexane (1:1) containing 0-5% Et_3NH as the eluting solvent. The pure product fractions are evaporated to give the title compound.

N4-Benzoyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine-3'-amidite

[00132] N4-Benzoyl-2'-O-methoxyethyl-5'-O-dimethoxytrityl-5-methylcytidine (74 g, 0.10 M) is dissolved in CH_2Cl_2 (1 L) Tetrazole diisopropylamine (7.1 g) and 2-cyanoethoxy-tetra(isopropyl)phosphite (40.5 mL, 0.123 M) are added with stirring, under a nitrogen atmosphere. The resulting mixture is stirred for 20 hours at room temperature (TLC showed the reaction to be 95% complete). The reaction mixture is extracted with saturated $NaHCO_3$ (1x300 mL) and saturated NaCl (3x300 mL). The aqueous washes are back-extracted with CH_2Cl_2 (300 mL), and the extracts are combined, dried over $MgSO_4$, and concentrated. The residue obtained is chromatographed on a 1.5 kg silica column using EtOAc/hexane (3:1) as the eluting solvent. The pure fractions were combined to give the title compound.

2'-O-(Aminooxyethyl) nucleoside amidites and 2'-O-(dimethylaminooxyethyl) nucleoside amidites
2'-(Dimethylaminooxyethoxy) nucleoside amidites

[00133] 2'-(Dimethylaminooxyethoxy) nucleoside amidites [also known in the art as 2'-O-(dimethylaminooxyethyl) nucleoside amidites] are prepared as described in the following paragraphs. Adenosine, cytidine and guanosine nucleoside amidites are prepared similarly to the thymidine (5-methyluridine) except the exocyclic amines are protected with a benzoyl moiety in the case of adenosine and cytidine and with isobutyryl in the case of guanosine.

5'-O-tert-Butyldiphenylsilyl -O^2 -2'-anhydro-5-methyluridine

[00134] O^2 -2'-anhydro-5-methyluridine (Pro. Bio. Sint., Varese, Italy, 100.0g, 0.4'6 mmol), dimethylaminopyridine (0.66g, 0.013eq, 0.0054mmol) are dissolved in dry pyridine (500 ml) at ambient temperature under an argon atmosphere and with mechanical stirring tert-Butyldiphenylchlorosilane (125.8g, 119.0mL, 1.1eq, 0.458mmol) is added in one portion. The reaction is stirred for 16 h at ambient temperature. TLC (Rf 0.22, ethyl acetate) indicated a complete reaction. The solution is concentrated under reduced pressure to a thick oil. This is partitioned between dichloromethane (1 L) and saturated sodium bicarbonate (2xl L) and brine (1 L). The organic layer is dried over sodium sulfate and concentrated under reduced pressure to a thick oil. The oil is dissolved in a 1:1 mixture of ethyl acetate and ethyl ether (600mL) and the solution is cooled to –10°C. The resulting crystalline product is collected by filtration, washed with ethyl ether (3x200 mL), and dried (40°C, 1mm Hg, 24 h) to a white solid.

5'-O-tert-Butyldiphenylsilyl-2'-O-(2-hydroxyethyl)-5-methyluridine

[00135] In a 2 L stainless steel, unstirred pressure reactor is added borane in tetrahydrofuran (1.0 M, 2.0 eq, 622 mL). In the fume hood and with manual stirring, ethylene glycol (350 mL, excess) is added cautiously at first until the evolution of hydrogen gas subsides. 5'-O-tert-Butyldiphenylsilyl-O^2-2'anhydro-5-methyluridine (149 g, 0.3'1 mol) and sodium bicarbonate (0.074 g, 0.003 eq) are added with manual stirring. The reactor is sealed and heated in an oil bath until an internal temperature of 160°C is reached and then maintained for 16 h (pressure < 100 psig). The reaction vessel is cooled to ambient and opened. TLC (Rf 0.67 for desired product and Rf 0.82 for ara-T side product, ethyl acetate)

indicated about 70% conversion to the product. In order to avoid additional side product formation, the reaction is stopped, concentrated under reduced pressure (10 to 1mm, Hg) in a warm water bath (40-100°C) with the more extreme conditions used to remove the ethylene glycol. [Alternatively, once the low boiling solvent is gone, the remaining solution can be partitioned between ethyl acetate and water. The product will be in the organic phase.] The residue is purified by column chromatography (2kg silica gel, ethyl acetate-hexanes gradient 1:1 to 4:1). The appropriate fractions are combined, stripped, and dried to product as a white crisp foam, contaminated starting material, and pure reusable starting material.

2'-O-([2-phthalimidoxy)ethyl]-5'-t-butyldiphenylsilyl-5-methyluridine

[00136] 5'-O-tert-Butyldiphenylsilyl-2'-O-(2-hydroxyethyl)-5-methyluridine (20g, 36.98mmol) is mixed with triphenylphosphine (11.63g, 44.36mmol) and N-hydroxyphthalimide (7.24g, 44.36mmol). It is then dried over P_2O_5 under high vacuum for two days at 40°C. The reaction mixture is flushed with argon and dry THF (369.8mL, Aldrich, sure seal bottle) is added to get a clear solution. Diethyl-azodicarboxylate (6.98mL, 44.36mmol) is added dropwise to the reaction mixture. The rate of addition is maintained such that resulting deep red coloration is just discharged before adding the next drop. After the addition is complete, the reaction is stirred for 4 hrs. By that time TLC showed the completion of the reaction (ethylacetate:hexane, 60:40). The solvent is evaporated in vacuum. Residue obtained is placed on a flash column and eluted with ethyl acetate:hexane (60:40), to get 2'-O-([2-phthalimidoxy)ethyl]-5'-t-butyldiphenylsilyl-5-methyluridine as white foam.

5'-O-tert-butyldiphenylsilyl-2'-O-[(2-formadoximinooxy)ethyl]-5-methyluridine

[00137] 2'-O-([2-phthalimidoxy)ethyl]-5'-t-butyldiphenylsilyl-5-methyluridine (3.1g, 4.5mmol) is dissolved in dry CH_2C1_2 (4.5mL) and methylhydrazine (300mL, 4.64mmol) is added dropwise at –10°C to 0°C. After 1 h the mixture is filtered, the filtrate is washed with ice cold CH_2Cl_2 and the combined organic phase is washed with water, brine and dried over anhydrous

Na_2SO_4. The solution is concentrated to get 2'-O(aminooxyethyl) thymidine, which is then dissolved in MeOH (67.5mL). To this formaldehyde (20% aqueous solution, w/w, 1.1 eq.) is added and the resulting mixture is stirred for 1 h. Solvent is removed under vacuum; residue chromatographed to get 5'-O-tert-butyldiphenylsilyl-2'-O-[(2-formadoximinooxy) ethyl]-5-methyluridine as white foam.

5'-O-tert-Butyldiphenylsilyl-2'-O-[N,N-dimethylaminooxyethyl]-5-methyluridine

[00138] 5'-O-tert-butyldiphenylsilyl-2'-O-[(2- formadoximinooxy)ethyl]-5-methyluridine (1.77g, 3.12mmol) is dissolved in a solution of 1M pyridinium p-toluenesulfonate (PPTS) in dry MeOH (30.6mL). Sodium cyanoborohydride (0.39g, 6.13mmol) is added to this solution at 10°C under inert atmosphere. The reaction mixture is stirred for 10 minutes at 10°C. After that the reaction vessel is removed from the ice bath and stirred at room temperature for 2 h, the reaction monitored by TLC (5% MeOH in CH_2Cl_2). Aqueous $NaHCO_3$ solution (5%, 10mL) is added and extracted with ethyl acetate (2x20mL). Ethyl acetate phase is dried over anhydrous Na_2SO_4, evaporated to dryness. Residue is dissolved in a solution of 1M PPTS in MeOH (30.6mL). Formaldehyde (20% w/w, 30mL, 3.37mmol) is added and the reaction mixture is stirred at room temperature for 10 minutes. Reaction mixture cooled to 10°C in an ice bath, sodium cyanoborohydride (0.39g, 6.13mmol) is added, and reaction mixture stirred at 10°C for 10 minutes. After 10 minutes, the reaction mixture is removed from the ice bath and stirred at room temperature for 2 hrs. To the reaction mixture 5% $NaHCO_3$ (25mL) solution is added and extracted with ethyl acetate (2x25mL). Ethyl acetate layer is dried over anhydrous Na_2SO_4 and evaporated to dryness. The residue obtained is purified by flash column chromatography and eluted with 5% MeOH in CH_2Cl_2 to get 5'-O-tertbutyldiphenylsilyl-2'-O-[N,N-dimethylaminooxyethyl]-5- methyluridine as a white foam.

2'-O-(dimethylaminooxyethyl)-5-methyluridine

[00139] Triethylamine trihydrofluoride (3.91mL, 24.0mmol) is dissolved in dry THF and triethylamine (1.67mL, 12mmol, dry, kept over KOH). This mixture of triethylamine-2HF is then added to 5'-O-tert-butyldiphenylsilyl-2'-O-[N,N-dimethylaminooxyethyl]-5-methyluridine (1.40g, 2.4mmol) and stirred at room temperature for 24 hrs. Reaction is monitored by TLC (5% MeOH in CH_2Cl_2). Solvent is removed under vacuum and the residue placed on a flash column and eluted with 10% MeOH in CH_2Cl_2 to get 2'-O-(dimethylaminooxyethyl)-5-methyluridine.

5'-O-DMT-2'-O-(dimethylaminooxyethyl)-5-methyluridine

[00140] 2'-O-(dimethylaminooxyethyl)-5-methyluridine (750mg, 2.17mmol) is dried over P_2O_5 under high vacuum overnight at 40°C. It is then co-evaporated with anhydrous pyridine (20mL). The residue obtained is dissolved in pyridine (11mL) under argon atmosphere. 4-dimethylaminopyridine (26.5mg, 2.60mmol), 4,4'-dimethoxytrityl chloride (880mg, 2.60mmol) is added to the mixture and the reaction mixture is stirred at room temperature until all of the starting material disappeared. Pyridine is removed under vacuum and the residue chromatographed and eluted with 10% MeOH in CH_2C1_2 (containing a few drops of pyridine) to get 5'-O-DMT-2'-0(dimethylamino-oxyethyl)-5-methyluridine.

5'-O-DMT-2'-O-(2-N,N-dimethylaminooxyethyl)-5-methyluridine-3'-[(2-cyanoethyl)-N,N- diisopropylphosphoramidite]

[00141] 5'-O-DMT-2'-O-(dimethylaminooxyethyl)-5-methyluridine (1.08g, 1.67mmol) is co-evaporated with toluene (20mL). To the residue N,N-diisopropylamine tetrazonide (0.29g, 1.67mmol) is added and dried over P20, under high vacuum overnight at 40°C. Then the reaction mixture is dissolved in anhydrous acetonitrile (8.4mL) and 2-cyanoethyl-N,N,N^1,N^1-tetraisopropylphosphoramidite (2.12mL, 6.08mmol) is added. The reaction mixture is stirred at ambient temperature for 4 hrs under inert atmosphere. The progress of the reaction is monitored by TLC (hexane:ethyl acetate 1:1). The solvent is evaporated, then the residue is dissolved in ethyl acetate (70mL) and

washed with 5% aqueous $NaHCO_3$ (40mL). Ethyl acetate layer is dried over anhydrous Na_2SO_4 and concentrated. Residue obtained is chromatographed (ethyl acetate as eluent) to get 5'-O-DMT-2'-O-(2-N,N-dimethylaminooxyethyl)-5-methyluridine-3'-[(2-cyanoethyl)-N,N-diisopropylphosphoramidite] as a foam.

2'-(Aminooxyethoxy) nucleoside amidites

[00142] 2'-(Aminooxyethoxy) nucleoside amidites [also known in the art as 2'-O-(aminooxyethyl) nucleoside amidites] are prepared as described in the following paragraphs. Adenosine, cytidine and thymidine nucleoside amidites are prepared similarly.

N2-isobutyryl-6-O-diphenylcarbamoyl-2'-O-(2-ethylacetyl)-5'-O-(4,4'-dimethoxytrityl)guanosine-3'-[(2-cyanoethyl)-N,N-diisopropylphosphoramidite]

[00143] The 2'-O-aminooxyethyl guanosine analog may be obtained by selective 2'-O-alkylation of diaminopurine riboside. Multigram quantities of diaminopurine riboside may be purchased from Schering AG (Berlin) to provide 2'-O-(2-ethylacetyl) diaminopurine riboside along with a minor amount of the 3'-O-isomer. 2'-O-(2-ethylacetyl) diaminopurine riboside may be resolved and converted to 2'-O-(2ethylacetyl)guanosine by treatment with adenosine deaminase. (McGee, D. P. C., Cook, P. D., Guinosso, C. J., WO 94/02501 Al 940203.) Standard protection procedures should afford 2'-O-(2-ethylacetyl)-5'-O-(4,4'-dimethoxytrityl)guanosine and 2-N-isobutyryl-6-O-diphenylcarbamoyl-2'-O-(2-ethylacetyl)-5'-O-(4,4'-dimethoxytrityl)guanosine which may be reduced to provide 2-N-isobutyryl-6-O-diphenylcarbamoyl-2'-O-(2-ethylacetyl)-5'-O-(4,4'-dimethoxytrityl)guanosine. As before the hydroxyl group may be displaced by N-hydroxyphthalimide via a Mitsunobu reaction, and the protected nucleoside may phosphitylated as usual to yield 2-N-isobutyryl-6-O-diphenylcarbamoyl-2'-O-(2-ethylacetyl)-5'-O-(4,4'-dimethoxytrityl)guanosine-3'-[(2-cyanoethyl)-N,N-diisopropylphosphoramiditel.

2'-dimethylaminoethoxyethoxy (2'-DMAEOE) nucleoside amidites

[00144] 2'-dimethylaminoethoxyethoxy nucleoside amidites (also known in the art as 2'-O-dimethylaminoethoxyethyl, i.e., 2'O-CH_2-O-CH_2-N(CH_2)$_2$, or 2'-DMAEOE nucleoside amidites) are prepared as follows. Other nucleoside amidites are prepared similarly.

2'-O-[2(2-N,N-dimethylaminoethoxy)ethyl]-5-methyl uridine

[00145] 2[2-(Dimethylamino)ethoxylethanol (Aldrich, 6.66 g, 50 mmol) is slowly added to a solution of borane in tetrahydrofuran (1 M, 10 mL, 10 mmol) with stirring in a 100 mL bomb. Hydrogen gas evolves as the solid dissolves. O^2-, 2' - anhydro-5-methyluridine (1.2 g, 5 mmol), and sodium bicarbonate (2.5 mg) are added and the bomb is sealed, placed in an oil bath, and heated to 155°C for 26 hours. The bomb is cooled to room temperature and opened. The crude solution is concentrated and the residue partitioned between water (200 mL) and hexanes (200 mL). The excess phenol is extracted into the hexane layer. The aqueous layer is extracted with ethyl acetate (3x200 mL) and the combined organic layers are washed once with water, dried over anhydrous sodium sulfate, and concentrated. The residue is columned on silica gel using methanol/methylene chloride 1:20 (which has 2% triethylamine) as the eluent. As the column fractions are concentrated a colorless solid forms which is collected to give the title compound as a white solid.

5'-O-dimethoxytrityl-2'-O-[2(2-N,N-dimethylaminoethoxy) ethyl)]-5-methyl uridine

[00146] To 0.5 g (1.3 mmol) of 2'-O-[2(2-N,N-dimethylaminoethoxy)ethyl)1-5-methyl uridine in anhydrous pyridine (8 mL), triethylamine (0.36 mL) and dimethoxytrityl chloride (DMT-Cl, 0.87 g, 2 eq.) are added and stirred for 1 hour. The reaction mixture is poured into water (200 mL) and extracted with CH_2Cl_2 (2x200 mL). The combined CH_2Cl_2 layers are washed with saturated $NaHCO_3$ solution, followed by saturated NaCl solution, and dried over anhydrous sodium sulfate. Evaporation of the solvent followed by silica gel chromatography using MeOH: CH_2Cl_2:Et_3N (20:1, v/v, with 1% triethylamine) gives the title compound.

5'-O-Dimethoxytrityl-2'-O-[2(2-N,N-dimethylaminoethoxy)ethyl)]-5-methyl uridine-3'-O-(cyanoethyl-N,N-diisopropyl)phosphoramidite

[00147] Diisopropylaminotetrazolide (0.6 g) and 2-cyanoethoxyN,N-diisopropyl phosphoramidite (1.1 mL, 2 eq.) are added to a solution of 5'-O-dimethoxytrityl-2'-O-[2(2-N,N-dimethylaminoethoxy)ethyl)]-5-methyluridine (2.17 g, 3 mmol) dissolved in CH_2Cl_2 (20 mL) under an atmosphere of argon. The reaction mixture is stirred overnight and the solvent evaporated. The resulting residue is purified by silica gel flash column chromatography with ethyl acetate as the eluent to give the title compound.

Example 2

Oligonucleotide synthesis

[00148] Unsubstituted and substituted phosphodiester (P=O) oligonucleotides are synthesized on an automated DNA synthesizer (Applied Biosystems model 380B) using standard phosphoramidite chemistry with oxidation by iodine.

[00149] Phosphorothioates (P=S) are synthesized as for the phosphodiester oligonucleotides except the standard oxidation bottle is replaced by 0.2 M solution of 3H-1,2-benzodithiole-3-one 1,1-dioxide in acetonitrile for the stepwise thiation of the phosphite linkages. The thiation wait step is increased to 68 sec and is followed by the capping step. After cleavage from the CPG column and deblocking in concentrated ammonium hydroxide at 55°C (18 h), the oligonucleotides are purified by precipitating twice with 2.5 volumes of ethanol from a 0.5 M NaCl solution. Phosphinate oligonucleotides are prepared as described in U.S. Patent 5,508,270, herein incorporated by reference.

[00150] Alkyl phosphonate oligonucleotides are prepared as described in U.S. Patent 4,469,863, herein incorporated by reference.

[00151] 3'-Deoxy-3'-methylene phosphonate oligonucleotides are prepared as described in U.S. Patents 5,610,289 or 5,625,050, herein incorporated by reference.

[00152] Phosphoramidite oligonucleotides are prepared as described in U.S. Patent, 5,256,775 or U.S. Patent 5,366,878, herein incorporated by reference.

[00153] Alkylphosphonothioate oligonucleotides are prepared as described in WO 94/17093 and WO 94/02499 herein incorporated by reference.

[00154] 3'-Deoxy-3'-amino phosphoramidate oligonucleotides are prepared as described in U.S. Patent 5,476,925, herein incorporated by reference.

[00155] Phosphotriester oligonucleotides are prepared as described in U.S. Patent 5,023,243, herein incorporated by reference.

[00156] Borano phosphate oligonucleotides are prepared as described in U.S. Patents 5,130,302 and 5,177,198, both herein incorporated by reference.

Example 3

Oligonucleoside Synthesis

[00157] Methylenemethylimino linked oligonucleosides, also identified as MMI linked oligonucleosides, methylenedimethylhydrazo linked oligonucleosides, also identified as MDH linked oligonucleosides, and methylenecarbonylamino linked oligonucleosides, also identified as amide-3 linked oligonucleosides, and methyleneaminocarbonyl linked oligonucleosides, also identified as amide-4 linked oligonucleosides, as well as mixed backbone compounds having, for instance, alternating MMI and P=O or P=S linkages are prepared as described in U.S. Patents 5,378,825; 5,386,023; 5,489,677; 5,602,240; and 5,610,289, all of which are herein incorporated by reference.

[00158] Formacetal and thioformacetal linked oligonucleosides are prepared as described in U.S. Patents 5,264,562 and 5,264,564, herein incorporated by reference.

[00159] Ethylene oxide linked oligonucleosides are prepared as described in U.S. Patent 5,223,618, herein incorporated by reference.

Example 4

PNA Synthesis

[00160] Peptide nucleic acids (PNAs) are prepared in accordance with any of the various procedures referred to in *Peptide Nucleic Acids* (PNA): *Synthesis, Properties and Potential Applications, Bioorganic & Medicinal Chemistry*, 1996, 4, 523. They may also be prepared in accordance with U.S. Patents 5,539,082; 5,700,922; and 5,719,262, herein incorporated by reference.

Example 5

Synthesis of Chimeric Oligonucleotides

[00161] Chimeric oligonucleotides, oligonucleosides, or mixed oligonucleotides/oligonucleosides of the invention can be of several different types. These include a first type wherein the "gap" segment of linked nucleosides is positioned between 5' and 3' "wing" segments of linked nucleosides and a second "open end" type wherein the "gap" segment is located at either the 3' or the 5' terminus of the oligomeric compound. Oligonucleotides of the first type are also known in the art as "gapmers" or gapped oligonucleotides. Oligonucleotides of the second type are also known in the art as "hemimers" or "wingmers".

[2'-O-Me]--[2'-deoxy]--[2'-O-Me] Chimeric Phosphorothioate Oligonucleotides

[00162] Chimeric oligonucleotides having 2'-O-alkyl phosphorothioate and 2'-deoxy phosphorothioate oligonucleotide segments are synthesized using an Applied Biosystems automated DNA synthesizer Model 380B, as above. Oligonucleotides are synthesized using the automated synthesizer and 2'-deoxy-5'-dimethoxytrityl-3'-O-phosphoramidite for the DNA portion and 5'-dimethoxytrityl-2'-O-methyl-3'-O-phosphoramidite for 5' and 3' wings. The standard synthesis cycle is modified by increasing the wait step after the delivery of tetrazole and base to 600 s repeated four times for RNA and twice for 2'-O-methyl. The fully protected oligonucleotide is cleaved from the support and the phosphate group is deprotected in 3:1 ammonia/ethanol at room temperature overnight then lyophilized to dryness. Treatment in methanolic

ammonia for 24 hrs at room temperature is then done to deprotect all bases and sample is again lyophilized to dryness. The pellet is resuspended in 1M TBAF in THF for 24 hrs at room temperature to deprotect the 2' positions. The reaction is then quenched with 1M TEAA and the sample is then reduced to 1/2 volume by rotovac before being desalted on a G25 size exclusion column. The oligo recovered is then analyzed spectrophotometrically for yield and for purity by capillary electrophoresis and by mass spectrometry.

[2'-O-(2-Methoxyethyl)]--[2'-deoxy]--[2'-O-(Methoxyethyl)] Chimeric Phosphorothioate Oligonucleotides

[00163] [2'-O-(2-methoxyethyl)]--[2'-deoxy]—[-2'-O-(methoxyethyl)] chimeric phosphorothioate oligonucleotides are prepared as per the procedure above for the 2'-O-methyl chimeric oligonucleotide, with the substitution of phorothioate oligonucleotides are prepared as per the procedure abo 2'-O-(methoxyethyl) amidites for the 2'-O-methyl amidites.

[2'-O-(2-Methoxyethyl)Phosphodiester]--[2'-deoxy Phosphorothioate]--[2'-O-(2-Methoxyethyl)] Phosphodiester] Chimeric Oligonucleotides

[00164] [2'-O-(2-methoxyethyl phosphodiester]--[2'-deoxy phosphorothioate]--[2'-O-(methcixyethyl) phosphodiester] chimeric oligonucleotides are prepared as per the above procedure for the 2'-O-methyl chimeric oligonucleotide with the substitution of 2'-O-(methoxyethyl) amidites for the 2'-O-methyl amidites, oxidization with iodine to generate the phosphodiester internucleotide linkages within the wing portions of the chimeric structures and sulfurization utilizing 3,H-1,2 benzodithiole-3-one 1,1 dioxide (Beaucage Reagent) to generate the phosphorothioate internucleotide linkages for the center gap.

[00165] Other chimeric oligonucleotides, chimeric oligonucleosides, and mixed chimeric oligonucleotides/oligonucleosides are synthesized according to United States patent 5,623,065, herein incorporated by reference.

Example 6

Oligonucleotide Isolation

[00166] After cleavage from the controlled pore glass column (Applied Biosystems) and deblocking in concentrated ammonium hydroxide at 55°C for 18 hours, the oligonucleotides or oligonucleosides are purified by precipitation twice out of 0.5 M NaCl with 2.5 volumes ethanol. Synthesized oligonucleotides are analyzed by polyacrylamide gel electrophoresis on denaturing gels and judged to be at least 85% full-length material. The relative amounts of phosphorothioate and phosphodiester linkages obtained in synthesis are periodically checked by "P nuclear magnetic resonance spectroscopy, and for some studies oligonucleotides are purified by HPLC, as described by Chiang et al., *J. Biol. Chem.* 1991, 266, 18162-18171.

Example 7

Oligonucleotide Synthesis - 96 Well Plate Format

[00167] Oligonucleotides are synthesized via solid phase P(III) phosphoramidite chemistry on an automated synthesizer capable of assembling 96 sequences simultaneously in a standard 96 well format. Phosphodiester internucleotide linkages are afforded by oxidation with aqueous iodine. Phosphorothioate internucleotide linkages are generated by sulfurization utilizing 3,H-1,2 benzodithiole-3-one 1,1 dioxide (Beaucage Reagent) in anhydrous acetonitrile. Standard base-protected beta-cyanoethyldiisopropyl phosphoramidites can be purchased from commercial vendors (e.g. PE-Applied Biosystems, Foster City, CA, or Pharmacia, Piscataway, NJ). Non-standard nucleosides are synthesized as per known literature or patented methods. They are utilized as base protected betacyanoethyldiisopropyl phosphoramidites.

[00168] Oligonucleotides are cleaved from support and deprotected with concentrated NH_4OH at elevated temperature (55-60°C) for 12-16 hours and the released product then dried in vacuo. The dried product is then re-suspended in sterile water to afford a master plate from which all analytical and test plate samples are then diluted utilizing robotic pipettors.

Example 8

Oligonucleotide Analysis - 96 Well Plate Format

[00169] The concentration of oligonucleotide in each well is assessed by dilution of samples and UV absorption spectroscopy. The full-length integrity of the individual products is evaluated by capillary electrophoresis (CE) in either the 96 well format (Beckman P/ACE™ MDQ) or, for individually prepared samples, on a commercial CE apparatus (e.g., Beckman P/ACE™ 5000, ABI 270). Base and backbone composition is confirmed by mass analysis of the compounds utilizing electrospray-mass spectroscopy. All assay test plates are diluted from the master plate using single and multi-channel robotic pipettors. Plates are judged to be acceptable if at least 85% of the compounds on the plate are at least 85% full length.

Example 9

Cell culture and oligonucleotide treatment

[00170] The effect of antisense compounds on target nucleic acid expression can be tested in any of a variety of cell types provided that the target nucleic acid is present at measurable levels. This can be routinely determined using, for example, PCR or Northern blot analysis. The following 6 cell types are provided for illustrative purposes, but other cell types can be routinely used, provided that the target is expressed in the cell type chosen. This can be readily determined by methods routine in the art, for example Northern blot analysis, Ribonuclease protection assays, or RT-PCR.

T-24 cells:

[00171] The human transitional cell bladder carcinoma cell line T-24 is obtained from the American Type Culture Collection (ATCC) (Manassas, VA). T-24 cells are routinely cultured in complete McCoy's 5A basal media (Gibco/Life Technologies, Gaithersburg, MD) supplemented with 10% fetal calf serum (Gibco/Life Technologies, Gaithersburg, MD), penicillin 100 units per mL, and streptomycin 100 micrograms per mL (Gibco/Life Technologies, Gaithersburg, MD). Cells are routinely passaged by trypsinization and dilution

when they reached 90% confluence. Cells are seeded into 96-well plates (Falcon-Primaria #3872) at a density of 7000 cells/well for use in RT-PCR analysis.

[00172] For Northern blotting or other analysis, cells may be seeded onto 100 mm or other standard tissue culture plates and treated similarly, using appropriate volumes of medium and oligonucleotide.

A549 cells:

[00173] The human lung carcinoma cell line A549 can be obtained from the American Type Culture Collection (ATCC) (Manassas, VA). A549 cells are routinely cultured in DMEM basal media (Gibco/Life Technologies, Gaithersburg, MD) supplemented with 10% fetal calf serum (Gibco/Life Technologies, Gaithersburg, MD), penicillin 100 units per mL, and streptomycin 100 micrograms per mL (Gibco/Life Technologies, Gaithersburg, MD). Cells are routinely passaged by trypsinization and dilution when they reached 90% confluence.

NHDF cells:

[00174] Human neonatal dermal fibroblast (NHDF) can be obtained from the Clonetics Corporation (Walkersville MD). NHDFs are routinely maintained in Fibroblast Growth Medium (Clonetics Corporation, Walkersville MD) supplemented as recommended by the supplier. Cells are maintained for up to 10 passages as recommended by the supplier.

HEK cells:

[00175] Human embryonic keratinocytes (HEK) can be obtained from the Clonetics Corporation (Walkersville MD). HEKs are routinely maintained in Keratinocyte Growth Medium (Clonetics Corporation, Walkersville MD) formulated as recommended by the supplier. Cells are routinely maintained for up to 10 passages as recommended by the supplier.

MCF-7 cells:

[00176] The human breast carcinoma cell line MCF-7 is obtained from the American Type Culture Collection (Manassas, VA). MCF-7 cells are routinely cultured in DMEM low glucose (Gibco/Life Technologies, Gaithersburg, MD) supplemented with 10% fetal calf serum (Gibco/Life Technologies, Gaithersburg, MD). Cells are routinely passaged by trypsinization and dilution when they reached 90% confluence. Cells are seeded into 96-well plates (Falcon-Primaria #3872) at a density of 7000 cells/well for use in RT-PCR analysis.

[00177] For Northern blotting or other analyses, cells may be seeded onto 100 mm or other standard tissue culture plates and treated similarly, using appropriate volumes of medium and oligonucleotide.

LA4 cells:

[00178] The mouse lung epithelial cell line LA4 is obtained from the American Type Culture Collection (Manassas, VA). LA4 cells are routinely cultured in F12K medium (Gibco/Life Technologies, Gaithersburg, MD) supplemented with 15% fetal calf serum (Gibco/Life Technologies, Gaithersburg, MD). Cells are routinely passaged by trypsinization and dilution when they reached 90% confluence. Cells are seeded into 96-well plates (Falcon-Primaria #3872) at a density of 3000-6000 cells/ well for use in RT-PCR analysis.

[00179] For Northern blotting or other analyses, cells may be seeded onto 100 mm or other standard tissue culture plates and treated similarly, using appropriate volumes of medium and oligonucleotide.

Treatment with antisense compounds:

[00180] When cells reached 80% confluence, they are treated with oligonucleotide. For cells grown in 96-well plates, wells are washed once with 200 µL OPTI-MEM™-1 reduced-serum medium (Gibco BRL) and then treated with 130 µL of OPTI-MEM™-1 containing 3.75 µg/mL LIPOFECTIN™ (Gibco BRL) and the desired concentration of oligonucleotide. After 4-7 hours of treatment, the medium is replaced with fresh medium. Cells are harvested 16-24 hours after oligonucleotide treatment.

[00181] The concentration of oligonucleotide used varies from cell line to cell line. To determine the optimal oligonucleotide concentration for a particular cell line, the cells are treated with a positive control oligonucleotide at a range of concentrations.

Example 10

Analysis of oligonucleotide inhibition of GFAT expression

[00182] Antisense modulation of GFAT expression can be assayed in a variety of ways known in the art. For example, GFAT mRNA levels can be quantitated by, e.g., Northern blot analysis, competitive polymerase chain reaction (PCR), or real-time PCR (RT-PCR). Real-time quantitative PCR is presently preferred. RNA analysis can be performed on total cellular RNA or poly(A)+ mRNA. Methods of RNA isolation are taught in, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 1, pp. 4.1.1-4.2.9 and 4.5.1-4.5.3, John Wiley & Sons, Inc., 1993. Northern blot analysis is routine in the art and is taught in, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 1, pp. 4.2.1-4.2.9, John Wiley & Sons, Inc., 1996. Real-time quantitative (PCR) can be conveniently accomplished using the commercially available ABI PRISM™ 7700 Sequence Detection System, available from PE-Applied Biosystems, Foster City, CA and used according to manufacturer's instructions. Prior to quantitative PCR analysis, primer-probe sets specific to the target gene being measured are evaluated for their ability to be "multiplexed" with a GAPDH amplification reaction. In multiplexing, both the target gene and the internal standard gene GAPDH are amplified concurrently in a single sample. In this analysis, mRNA isolated from untreated cells is serially diluted. Each dilution is amplified in the presence of primer-probe sets specific for GAPDH only, target gene only ("single-plexing"), or both (multiplexing). Following PCR amplification, standard curves of GAPDH and target mRNA signal as a function of dilution are generated from both the single-plexed and multiplexed samples. If both the slope and correlation coefficient of the GAPDH and target signals generated from the multiplexed samples fall within 10% of their corresponding values

generated from the single-plexed samples, the primer-probe set specific for that target is deemed as multiplexable. Other methods of PCR are also known in the art.

[00183] Protein levels of GFAT can be quantitated in a variety of ways well known in the art, such as immunoprecipitation, Western blot analysis (immunoblotting), ELISA or fluorescence-activated cell sorting (FACS). Antibodies directed to GFAT can be identified and obtained from a variety of sources, such as the MSRS catalog of antibodies (Aerie Corporation, Birmingham, MI), or can be prepared via conventional antibody generation methods. Methods for preparation of polyclonal antisera are taught in, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 2, pp. 11.12.1-11.12.9, John Wiley & Sons, Inc., 1997. Preparation of monoclonal antibodies is taught in, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 2, pp. 11.4.1-11.11.5, John Wiley Sons, Inc., 1997.

[00184] Immunoprecipitation methods are standard in the art and can be found at, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 2, pp. 10.16.110.16.11, John Wiley & Sons, Inc., 1998. Western blot (immunoblot) analysis is standard in the art and can be found at, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 2, pp. 10.8.1-10.8.21, John Wiley Sons, Inc., 1997. Enzyme-linked immunosorbent assays (ELISA) are standard in the art and can be found at, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 2, pp. 11.2.1-11.2.22, John Wiley & Sons, Inc., 1991.

Example 11

Poly(A)+ mRNA isolation

[00185] Poly(A)+ mRNA is isolated according to Miura et al., *Clin. Chem.*, 1996, 42, 1758-1764. Other methods for poly(A)+ mRNA isolation are taught in, for example, Ausubel, F.M. et al., *Current Protocols in Molecular Biology*, Volume 1, pp. 4.5.1-4.5.3, John Wiley & Sons, Inc., 1993. Briefly, for cells grown on 96-well plates, growth medium is removed from the cells and

each well is washed with 200 µL cold PBS. 60µL lysis buffer (10 mM Tris-HCl, pH 7.6, 1 mM EDTA, 0.5 M NaCl, 0.5% NP-40, 20 mM vanadyl-ribonucleoside complex) is added to each well, the plate is gently agitated and then incubated at room temperature for five minutes. 55 µL of lysate is transferred to Oligo d(T) coated 96-well plates (AGCT Inc., Irvine CA). Plates are incubated for 60 minutes at room temperature, washed 3 times with 200 µL of wash buffer (10 mM Tris-HC1 pH 7.6, 1 mM EDTA, 0.3 M NaCl). After the final wash, the plate is blotted on paper towels to remove excess wash buffer and then air-dried for 5 minutes. 60 pL of elution buffer (5 mM Tris-HCl pH 7.6), preheated to 70°C is added to each well, the plate is incubated on a 90°C hot plate for 5 minutes, and the eluate is then transferred to a fresh 96-well plate.

[00186] Cells grown on 100 mm or other standard plates may be treated similarly, using appropriate volumes of all solutions.

Example 12

Total RNA Isolation

[00187] Total mRNA is isolated using an RNEASY 96™ kit and buffers purchased from Qiagen Inc. (Valencia CA) following the manufacturer's recommended procedures. Briefly, for cells grown on 96-well plates, growth medium is removed from the cells and each well is washed with 200 µL cold PBS. 100 µL Buffer RLT is added to each well and the plate vigorously agitated for 20 seconds. 100 µL of 70% ethanol is then added to each well and the contents mixed by pipetting three times up and down. The samples are then transferred to the RNEASY 96™ well plate attached to a QIAVAC™ manifold fitted with a waste collection tray and attached to a vacuum source. Vacuum is applied for 15 seconds. 1 mL of Buffer RW1 is added to each well of the RNEASY 96™ plate and the vacuum again applied for 15 seconds. 1 mL of Buffer RPE is then added to each well of the RNEASY 96™ plate and the vacuum applied for a period of 15 seconds. The Buffer RPE wash is then repeated and the vacuum is applied for an additional 10 minutes. The plate is then removed from the QIAVAC™ manifold and blotted dry on paper towels.

The plate is then re-attached to the QIAVAC™ manifold fitted with a collection tube rack containing 1.2 mL collection tubes. RNA is then eluted by pipetting 60μL water into each well, incubating one minute, and then applying the vacuum for 30 seconds. The elution step is repeated with an additional 60μL water.

[00188] The repetitive pipetting and elution steps may be automated using a QIAGEN Bio-Robot 9604 (Qiagen, Inc., Valencia CA). Essentially, after lysing of the cells on the culture plate, the plate is transferred to the robot deck where the pipetting, DNase treatment and elution steps are carried out.

Example 13

Real-time Quantitative PCR Analysis of GFAT mRNA Levels

[00189] Quantitation of GFAT mRNA levels is determined by real-time quantitative PCR using the ABI PRISM™ 7700 Sequence Detection System (PE-Applied Biosystems, Foster City, CA) according to manufacturer's instructions. This is a closed-tube, non-gel-based, fluorescence detection system which allows high-throughput quantitation of polymerase chain reaction (PCR) products in real-time. As opposed to standard PCR, in which amplification products are quantitated after the PCR is completed, products in real-time quantitative PCR are quantitated as they accumulate. This is accomplished by including in the PCR reaction an oligonucleotide probe that anneals specifically between the forward and reverse PCR primers, and contains two fluorescent dyes. A reporter dye (e.g., JOE, FAM™, or VIC, obtained from either Operon Technologies Inc., Alameda, CA or PE-Applied Biosystems, Foster City, CA) is attached to the 5' end of the probe and a quencher dye (e.g., TAMRA, obtained from either Operon Technologies Inc., Alameda, CA or PE-Applied Biosystems, Foster City, CA) is attached to the 3' end of the probe. When the probe and dyes are intact, reporter dye emission is quenched by the proximity of the 3' quencher dye. During amplification, annealing of the probe to the target sequence creates a substrate that can be cleaved by the 5'-exonuclease activity of Taq polymerase. During the extension phase of the PCR amplification cycle, cleavage of the probe by Taq polymerase releases the reporter dye from the

remainder of the probe (and hence from the quencher moiety) and a sequence-specific fluorescent signal is generated. With each cycle, additional reporter dye molecules are cleaved from their respective probes, and the fluorescence intensity is monitored at regular intervals by laser optics built into the ABI PRISM™ 7700 Sequence Detection System. In each assay, a series of parallel reactions containing serial dilutions of mRNA from untreated control samples generates a standard curve that is used to quantitate the percent inhibition after antisense oligonucleotide treatment of test samples.

[00190] PCR reagents can be obtained from PE-Applied Biosystems, Foster City, CA. RT-PCR reactions are carried out by adding 25μL PCR cocktail (1x TAQMAN™ buffer A, 5.5 MM $MgCl_2$, 300 μM each of dATP, dCTP and dGTP, 600 μM of dUTP, 100 nM each of forward primer, reverse primer, and probe, 20 Units RNAse inhibitor, 1.25 Units AMPLITAQ GOLD™, and 12.5 Units MuLV reverse transcriptase) to 96 well plates containing 25 μL poly(A) mRNA solution. The RT reaction is carried out by incubation for 30 minutes at 48°C. Following a 10 minute incubation at 95°C to activate the AMPLITAQ GOLD™, 40 cycles of a two-step PCR protocol are carried out: 95°C for 15 seconds (denaturation) followed by 60°C for 1.5 minutes (annealing/extension).

[00191] Probes and primers to human GFAT-1 were designed to hybridize to a human GFAT-1 sequence, using published sequence, information (GenBank accession number NM_002056, incorporated herein as Figure 1). For human GFAT-1 the PCR primers were:

forward primer: ATGCAAGAAAGACGCAAAGAGAT SEQ ID NO:3064

reverse primer: TTCGTCATCCATGCTCAGTACTTC SEQ ID NO:3065 and the PCR probe is:

FAM™- ATGCTTGGATTGAAACGGCTGCCTG SEQ ID NO:3066-TAMRA

where FAM™ (PE-Applied Biosystems, Foster City, CA) is the fluorescent reporter dye) and TAMRA (PE-Applied Biosystems, Foster City, CA) is the quencher dye. For human cyclophilin the PCR primers were:

forward primer: CCCACCGTGTTCTTCGACAT SEQ ID NO:3067

reverse primer: TTTCTGCTGTCTTTGGGACCTT SEQ ID NO:3068 and the PCR probe is: 5' JOE- CGCGTCTCCTTTGAGCTGTTTGCA SEQ ID NO:3069- TAMRA 3' where JOE (PE-Applied Biosystems, Foster City, CA) is the fluorescent reporter dye) and TAMRA (PE-Applied Biosystems, Foster City, CA) is the quencher dye.

Example 14

Antisense inhibition of human GFAT expression by chimeric phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap

[00192] In accordance with the present invention, a series of oligonucleotides are designed to target different regions of the human GFAT-1 RNA, using published sequences (GenBank accession number NM_002056, incorporated herein as Figure 1). The oligonucleotides are shown in Table 1. "Position" indicates the first (5'-most) nucleotide number on the particular target sequence to which the oligonucleotide binds. The indicated parameters for each oligo were predicted using RNAstructure 3.7 by David H. Mathews, Michael Zuker, and Douglas H. Turner. The parameters are described either as free energy (The energy that is released when a reaction occurs. The more negative the number, the more likely the reaction will occur. All free energy units are in kcal/mol.) or melting temperature (the temperature at which two anneal strands of polynucleic acid separate. The higher the temperature, greater the affinity between the 2 strands.) When designing an antisense oligonucleotide (oligomers) that will bind with high affinity, it is desirable to consider the structure of the target RNA strand and the antisense oligomer. Specifically, for an oligomer to bind tightly (in the table described as 'duplex formation'), it should be complementary to a stretch of target RNA that has little self-structure (in the table the free energy of which is described as 'target structure'). Also, the oligomer should have little self-structure, either intramolecular (in the table the free energy of which is described as 'intramolecular oligo') or bimolecular (in the table the free energy of which is described as 'intermolecular oligo'). Breaking up any self-structure amounts to a binding penalty. All compounds in Table 1 are chimeric oligonucleotides ("gapmers") 20 nucleotides in length, composed of a central "gap" region

consisting of ten 2'deoxynucleotides, which is flanked on both sides (5' and 3' directions) by four-nucleotide "wings". The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. The internucleoside (backbone) linkages are phosphorothioate (P=S) throughout the oligonucleotide. Cytidine residues in the 2'-MOE wings are 5-methylcytidines. All cytidine residues are 5-methylcytidines.

Table 1

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1986	ATGGTCTCAGTATCCTCCTT SEQ ID NO:1	-24.4	-26.4	78.1	-2	0	-3.2
12	GGGGGCCGGGGTGGCGCCGA SEQ ID NO:2	-24.3	-37.2	90.5	-11	-0.2	-12
1984	GGTCTCAGTATCCTCCTTAT SEQ ID NO:3	-24.1	-26.1	77.7	-2	0	-2.5
1985	TGGTCTCAGTATCCTCCTTA SEQ ID NO:4	-24.1	-26.1	77.6	-2	0	-3.2
15	CTCGGGGGCCGGGGTGGCGC SEQ ID NO:5	-23.8	-35.9	89.9	-11	3.5	-10.2
1987	AATGGTCTCAGTATCCTCCT SEQ ID NO:6	-23.6	-25.6	75	-2	0	-3.2
445	TTTATCAGAGCGCTGGGGGT SEQ ID NO:7	-23.4	-26.9	76.6	-2.5	-0.6	-9.4
14	TCGGGGGCCGGGGTGGCGCC SEQ ID NO:8	-23.3	-37	91.1	-11	0.9	-13.6
2246	GGCTTCAAGGGGTGATATTT SEQ ID NO:9	-23.1	-23.7	69.9	1	-0.3	-7.6
2247	AGGCTTCAAGGGGTGATATT SEQ ID NO:10	-23.1	-23.6	69.8	1	0	-7.6
2203	AGGTGTCTTGTGTTGCTTAA SEQ ID NO:11	-22.7	-23.3	71.3	-0.3	0	-3.6
2204	AAGGTGTCTTGTGTTGCTTA SEQ ID NO:12	-22.7	-23.3	71.3	-0.3	0	-3.6
17	GGCTCGGGGGCCGGGGTGGC SEQ ID NO:13	-22.5	-36.3	93.3	-11	-2.8	-9.2
1988	TAATGGTCTCAGTATCCTCC SEQ ID NO:14	-22.4	-24.4	72.4	-2	0	-3.2
2248	AAGGCTTCAAGGGGTGATAT SEQ ID NO:15	-22.2	-22.8	67.1	1	-0.3	-7.6
11	GGGGCCGGGGTGGCGCCGAC SEQ ID NO:16	-22.1	-36.2	88.8	-12.2	0.6	-12
88	GCCCGCGAGGCCAGGGGCGA SEQ ID NO:17	-22.1	-36.3	88	-10.8	-3.4	-13.4
446	TTTTATCAGAGCGCTGGGGG SEQ ID NO:18	-22	-25.8	73.5	-2.5	-1.2	-9.4
2202	GGTGTCTTGTGTTGCTTAAT SEQ ID NO:19	-22	-23.3	70.9	-1.2	0	-3.6
2245	GCTTCAAGGGGTGATATTTT SEQ ID NO:20	-22	-22.6	67.6	1	-0.3	-4.3
1784	CTTTGATTTTCAGTGCCCCT SEQ ID NO:21	-21.7	-27	76	-5.3	0	-3.8

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2205	AAAGGTGTCTTGTGTTGCTT SEQ ID NO:22	-21.6	-22.9	69.4	-0.3	-0.4	-4.3
16	GCTCGGGGGCCGGGGTGGCG SEQ ID NO:23	-21.5	-35.9	89.9	-11	-3.4	-9.2
2249	AAAGGCTTCAAGGGGTGATA SEQ ID NO:24	-21.5	-22.1	64.9	1	-0.3	-7.6
87	CCCGCGAGGCCAGGGGCGAG SEQ ID NO:25	-21.2	-34.5	84.4	-10.8	-2.5	-11.2
444	TTATCAGAGCGCTGGGGGTG SEQ ID NO:26	-21.2	-26.8	76	-4.3	-1.2	-9.4
1983	GTCTCAGTATCCTCCTTATC SEQ ID NO:27	-21.2	-25.3	76.8	-4.1	0	-1.4
2250	AAAAGGCTTCAAGGGGTGAT SEQ ID NO:28	-21.1	-21.7	63.4	1	-0.3	-7.6
20	GCGGGCTCGGGGGCCGGGGT SEQ ID NO:29	-21	-37.1	92.5	-12.5	-3.6	-9.5
1990	CTTAATGGTCTCAGTATCCT SEQ ID NO:30	-21	-23	69.3	-2	0	-4
1137	TTGACTCTTCCTCTCATTGT SEQ ID NO:31	-20.8	-24.2	72.9	-3.4	0	-2.6
1138	GTTGACTCTTCCTCTCATTG SEQ ID NO:32	-20.8	-24.2	72.9	-3.4	0	-2.6
1139	AGTTGACTCTTCCTCTCATT SEQ ID NO:33	-20.8	-24.2	73.4	-3.4	0	-3.8
2206	AAAAGGTGTCTTGTGTGCT SEQ ID NO:34	-20.8	-22.1	66.6	-0.3	-0.4	-4.3
1136	TGACTCTTCCTCTCATTGTG SEQ ID NO:35	-20.7	-24.1	72.3	-3.4	0	-2.4
1312	GTCACTTGCTAGTTCCACCA SEQ ID NO:36	-20.6	-27.2	78.3	-6.6	0	-1.7
90	CGGCCCGCGAGGCCAGGGGC SEQ ID NO:37	-20.5	-36.9	89.1	-11.5	-4.7	-17.4
1989	TTAATGGTCTCAGTATCCTC SEQ ID NO:38	-20.5	-22.5	68.9	-2	0	-4
1991	TCTTAATGGTCTCAGTATCC SEQ ID NO:39	-20.5	-22.5	68.9	-2	0	-2.6
2207	CAAAAGGTGTCTTGTGTTGC SEQ ID NO:40	-20.5	-21.9	65.8	-0.3	-0.6	-3.8
86	CCGCGAGGCCAGGGGCGAGT SEQ ID NO:41	-20.4	-33.7	84.6	-10.8	-2.5	-11.2
1051	GATCTGCTGGAGTTCCATCT SEQ ID NO:42	-20.4	-26.1	76.7	-5.1	-0.3	-6.3
1781	TGATTTTCAGTGCCCCTTCA SEQ ID NO:43	-20.4	-27.1	76.5	-6.7	0	-3.8
13	CGGGGGCCGGGGTGGCGCCG SEQ ID NO:44	-20.3	-37.4	88.6	-14.2	-0.2	-14
322	AACTTCTTCATCCAGTGCCT SEQ ID NO:45	-20.3	-26	74.7	-5.7	0	-3.6
438	GAGCGCTGGGGGTGGCTATT SEQ ID NO:46	-20.1	-29.6	81.9	-8.5	-0.8	-9.4
1140	AAGTTGACTCTTCCTCTCAT SEQ ID NO:47	-20	-23.4	70.4	-3.4	0	-4.5
2869	TCAGTTGTCCAAAGCAGCTT SEQ ID NO:48	-20	-24.6	71.9	-3.9	-0.4	-8.1
18	GGGCTCGGGGGCCGGGGTGG SEQ ID NO:49	-19.9	-35.7	91.4	-12.2	-3.6	-9.2
447	TTTTTATCAGAGCGCTGGGG SEQ ID NO:50	-19.9	-24.7	71.3	-3.5	-1.2	-9.4
1313	AGTCACTTGCTAGTTCCACC SEQ ID NO:51	-19.9	-26.5	77.5	-6.6	0	-1.7

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1782	TTGATTTTCAGTGCCCCTTC SEQ ID NO:52	-19.9	-26.5	75.8	-6.6	0	-3.8
21	TGCGGGCTCGGGGGCCGGGG SEQ ID NO:53	-19.8	-35.9	88.9	-12.5	-3.6	-11.8
437	AGCGCTGGGGGTGGCTATTG SEQ ID NO:54	-19.8	-29	80.3	-8.5	-0.3	-8.7
854	CCACCGGGAAAAGGCAGGTT SEQ ID NO:55	-19.8	-26.8	71	-6.5	-0.1	-7.1
321	ACTTCTTCATCCAGTGCCTT SEQ ID NO:56	-19.7	-26.8	77.7	-7.1	0	-3.6
855	TCCACCGGGAAAAGGCAGGT SEQ ID NO:57	-19.7	-27.1	72.1	-6.5	-0.8	-7.1
485	TGGTGATGATTCCATTGTGA SEQ ID NO:58	-19.6	-22.7	67.2	-2.5	-0.3	-3.9
1586	CATCACACATCATAAGGGCA SEQ ID NO:59	-19.6	-22.6	65.7	-3	0	-4
1592	TCCGATCATCACACATCATA SEQ ID NO:60	-19.6	-22.6	65.5	-3	0	-4.9
2868	CAGTTGTCCAAAGCAGCTTG SEQ ID NO:61	-19.6	-24.2	70.1	-3.9	-0.4	-8.4
323	GAACTTCTTCATCCAGTGCC SEQ ID NO:62	-19.5	-25.7	74.1	-5.7	-0.2	-4
1052	TGATCTGCTGGAGTTCCATC SEQ ID NO:63	-19.5	-25.2	74.4	-5.1	-0.3	-6.3
2867	AGTTGTCCAAAGCAGCTTGA SEQ ID NO:64	-19.5	-24.1	70.3	-3.9	-0.3	-8.4
439	AGAGCGCTGGGGGTGGCTAT SEQ ID NO:65	-19.4	-29.5	81.8	-9.1	-0.8	-9.4
1310	CACTTGCTAGTTCCACCATC SEQ ID NO:66	-19.4	-26	74.6	-6.6	0	-1.7
1311	TCACTTGCTAGTTCCACCAT SEQ ID NO:667	-19.4	-26	74.6	-6.6	0	-1.7
1141	AAAGTTGACTCTTCCTCTCA SEQ ID NO:68	-19.3	-22.7	68	-3.4	0	-4.5
1142	CAAAGTTGACTCTTCCTCTC SEQ ID NO:69	-19.3	-22.7	68	-3.4	0	-4.5
1143	TCAAAGTTGACTCTTCCTCT SEQ ID NO:70	-19.3	-22.7	68	-3.4	0	-5.1
1587	TCATCACACATCATAAGGGC SEQ ID NO:71	-19.3	-22.3	66.1	-3	0	-2.9
1982	TCTCAGTATCCTCCTTATCA SEQ ID NO:72	-19.2	-24.8	74.2	-5.6	0	-1.6
487	GTTGGTGATGATTCCATTGT SEQ ID NO:73	-19.1	-23.4	69.7	-3.6	-0.5	-4.9
443	TATCAGAGCGCTGGGGGTGG SEQ ID NO:74	-19	-27.9	78.3	-7.6	-1.2	-9.4
1047	TGCTGGAGTTCCATCTGGAG SEQ ID NO:75	-19	-26	75.7	-6.4	-0.3	-6.9
1129	TCCTCTCATTGTGTTCACGA SEQ ID NO:76	-18.9	-25	73	-6.1	0	-6.4
2201	GTGTCTTGTGTTGCTTAATC SEQ ID NO:77	-18.9	-22.5	69.8	-3.6	0	-3.6
2252	AAAAAAGGCTTCAAGGGGTG SEQ ID NO:78	-18.9	-19.7	58.3	-0.6	0	-4.6
2866	GTTGTCCAAAGCAGCTTGAA SEQ ID NO:79	-18.9	-23.4	67.7	-3.9	0	-8.4
9	GGCCGGGGTGGCGCCGACAC SEQ ID NO:80	-18.8	-34.7	85.6	-12.5	-3.4	-12.1
1064	AGTTGCCCTTCATGATCTGC SEQ ID NO:81	-18.8	-26.9	77.2	-8.1	0	-6.4

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1780	GATTTTCAGTGCCCCTTCAA SEQ ID NO:82	-18.8	-26.4	74.2	-7.6	0	-3.8
1783	TTTGATTTTCAGTGCCCCTT SEQ ID NO:83	-18.7	-26.2	74.5	-7.5	0	-3.8
320	CTTCTTCATCCAGTGCCTTA SEQ ID NO:84	-18.6	-26.3	76.5	-7.7	0	-3.6
1992	TTCTTAATGGTCTCAGTATC SEQ ID NO:85	-18.6	-20.6	65.2	-2	0	-2.6
2253	AAAAAAAGGCTTCAAGGGGT SEQ ID NO:86	-18.6	-19	56.6	1.6	0	-3.7
10	GGGCCGGGGTGGCGCCGACA SEQ ID NO:87	-18.5	-35.7	87.4	-13.8	-3.4	-12.1
488	AGTTGGTGATGATTCCATTG SEQ ID NO:88	-18.5	-22.2	66.6	-3	-0.5	-4.9
1131	CTTCCTCTCATTGTGTTCAC SEQ ID NO:89	-18.5	-24.6	74.2	-6.1	0	-4.9
1591	CCGATCATCACACATCATAA SEQ ID NO:90	-18.5	-21.5	62.1	-3	0	-4.9
1593	ATCCGATCATCACACATCAT SEQ ID NO:91	-18.5	-22.9	66	-4.4	0	-4.9
85	CGCGAGGCCAGGGGCGAGTG SEQ ID NO:92	-18.4	-31.7	81.3	-10.8	-2.5	-10.4
1130	TTCCTCTCATTGTGTTCACG SEQ ID NO:93	-18.4	-24.5	72	-6.1	0	-6.3
1788	ATTTCTTTGATTTTCAGTGC SEQ ID NO:94	-18.4	-20.7	64.9	-2.3	0	-3.8
404	CTCCATGTGTTGCCCAACGG SEQ ID NO:95	-18.3	-28.5	75.7	-9.3	-0.8	-7.7
1133	CTCTTCCTCTCATTGTGTTC SEQ ID NO:96	-18.3	-25	76.4	-6.7	0	-2.4
1134	ACTCTTCCTCTCATTGTGTT SEQ ID NO:97	-18.3	-24.8	75.2	-6.5	0	-2.4
1309	ACTTGCTAGTTCCACCATCA SEQ ID NO:98	-18.3	-26	74.6	-7.7	0	-1.4
1319	CCAGGAAGTCACTTGCTAGT SEQ ID NO:99	-18.3	-24.9	72.7	-6.6	0	-1.4
91	ACGGCCCGCGAGGCCAGGGG SEQ ID NO:100	-18.2	-35.3	85.7	-12.2	-4.7	-17.4
409	GGGTTCTCCATGTGTTGCCC SEQ ID NO:101	-18.2	-30.4	85.3	-10.9	-1.2	-4.8
489	TAGTTGGTGATGATTCCATT SEQ ID NO:102	-18.2	-21.9	66.1	-3	-0.5	-4.1
547	GTCTGTTTCAGATTCGAAGT SEQ ID NO:103	-18.2	-22	67.2	-2.2	-1.4	-10.4
1060	GCCCTTCATGATCTGCTGGA SEQ ID NO:104	-18.2	-28.3	78.9	-10.1	0	-6.1
1145	CATCAAAGTTGACTCTTCCT SEQ ID NO:105	-18.2	-22.1	65.7	-3.4	-0.1	-6
1585	ATCACACATCATAAGGGCAA SEQ ID NO:106	-18.2	-21.2	62.5	-3	0	-4
2871	TGTCAGTTGTCCAAAGCAGC SEQ ID NO:107	-18.2	-24.8	72.8	-6.6	0	-4.1
158	TTTCTCGTCTCGTTCGAGGA SEQ ID NO:108	-18.1	-25.3	73	-4.7	-2.5	-9.1
1132	TCTTCCTCTCATTGTGTTCA SEQ ID NO:109	-18.1	-24.8	75.4	-6.7	0	-3.4
1315	GAAGTCACTTGCTAGTTCCA SEQ ID NO:110	-18.1	-24.2	71.8	-6.1	0	-1.7
1316	GGAAGTCACTTGCTAGTTCC SEQ ID NO:111	-18.1	-24.7	73.4	-6.6	0	-1.8

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2514	CTGGTCTGAATGAAGTATGG SEQ ID NO:112	-18.1	-20.5	62.1	-2.4	0	-3
2872	TTGTCAGTTGTCCAAAGCAG SEQ ID NO:113	-18.1	-23.1	68.7	-5	0	-4.1
2873	ATTGTCAGTTGTCCAAAGCA SEQ ID NO:115	-18.1	-23.1	68.4	-5	0	-4.1
436	GCGCTGGGGGTGGCTATTGA SEQ ID NO:115	-18	-29.6	81.3	-11.1	-0.2	-7.2
19	CGGGCTCGGGGGCCGGGGTG SEQ ID NO:116	-17.9	-35.3	88.2	-13.8	-3.6	-9.2
34	TCGGTGGGCAATCTGCGGGC SEQ ID NO:117	-17.9	-29.9	80	-9.8	-2.2	-7
546	TCTGTTTCAGATTCGAAGTC SEQ ID NO:118	-17.9	-21.2	65.3	-2.2	-0.9	-9.3
1144	ATCAAAGTTGACTCTTCCTC SEQ ID NO:119	-17.9	-21.8	66	-3.4	-0.1	-6
2863	GTCCAAAGCAGCTTGAATTT SEQ ID NO:120	-17.9	-22.3	65	-3.9	0	-7.9
160	GATTTCTCGTCTCGTTCGAG SEQ ID NO:121	-17.8	-24.1	70.3	-4.7	-1.5	-8.5
161	GGATTTCTCGTCTCGTTCGA SEQ ID NO:122	-17.8	-25.3	72.7	-6.8	-0.4	-5.2
484	GGTGATGATTCCATTGTGAA SEQ ID NO:123	-17.8	-22	65.1	-3.5	-0.5	-4
534	TCGAAGTCATAGCCTTTGCT SEQ ID NO:124	-17.8	-24.7	71	-5.7	-1.1	-6.4
406	TTCTCCATGTGTTGCCCAAC SEQ ID NO:125	-17.7	-27	75.5	-9.3	0	-6.3
442	ATCAGAGCGCTGGGGGTGGC SEQ ID NO:126	-17.7	-30	83.4	-11	-1.2	-8.8
856	TTCCACCGGGAAAAGGCAGG SEQ ID NO:127	-17.7	-26	69.5	-6.5	-1.8	-7.6
1044	TGGAGTTCCATCTGGAGTGT SEQ ID NO:128	-17.7	-25.7	76.4	-7.5	-0.2	-6.9
1146	TCATCAAAGTTGACTCTTCC SEQ ID NO:129	-17.7	-21.6	65.2	-3.4	-0.1	-6
1314	AAGTCACTTGCTAGTTCCAC SEQ ID NO:130	-17.7	-23.8	71.1	-6.1	0	-1.5
1533	GCCTTTGTACTGGCCACACC SEQ ID NO:131	-17.7	-29.7	80.7	-10.8	-1.1	-8.4
2864	TGTCCAAAGCAGCTTGAATT SEQ ID NO:132	-17.7	-22.2	64.6	-3.9	0	-8.4
2865	TTGTCCAAAGCAGCTTGAAT SEQ ID NO:133	-17.7	-22.2	64.6	-3.9	0	-8.4
448	ATTTTTATCAGAGCGCTGGG SEQ ID NO:134	-17.6	-23.5	68.7	-4.6	-1.2	-9.4
535	TTCGAAGTCATAGCCTTTGC SEQ ID NO:135	-17.6	-23.9	69.4	-5.7	-0.3	-6.8
858	TCTTCCACCGGGAAAAGGCA SEQ ID NO:136	-17.6	-26.1	70.1	-6.5	-2	-7.9
1061	TGCCCTTCATGATCTGCTGG SEQ ID NO:137	-17.6	-27.7	77.4	-10.1	0	-6.8
89	GGCCCGCGAGGCCAGGGGCG SEQ ID NO:138	-17.5	-36.9	89.1	-14.7	-4.2	-17.2
159	ATTTCTCGTCTCGTTCGAGG SEQ ID NO:139	-17.5	-24.7	71.6	-4.7	-2.5	-9.1
385	GGTATGAGCTATTCCAAGGT SEQ ID NO:140	-17.5	-24	70.7	-6.5	0	-5.1
405	TCTCCATGTGTTGCCCAACG SEQ ID NO:141	-17.5	-27.7	74.9	-9.3	-0.8	-7.7

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
723	AGAGGGCTACCTCGCCTTGT SEQ ID NO:142	-17.5	-29.7	81.6	-8.3	-3.9	-9.6
866	CTGCTTTTTCTTCCACCGGG SEQ ID NO:143	-17.5	-27.9	76.8	-10.4	0	-7.1
1584	TCACACATCATAAGGGCAAA SEQ ID NO:144	-17.5	-20.5	60.5	-3	0	-4
1588	ATCATCACACATCATAAGGG SEQ ID NO:145	-17.5	-20.5	61.9	-3	0	-1.7
1790	TAATTTCTTTGATTTTCAGT SEQ ID NO:146	-17.5	-17.9	57.8	0.2	0	-2.8
1791	GTAATTTCTTTGATTTTCAG SEQ ID NO:147	-17.5	-17.9	57.8	0.6	0	-2.8
1792	AGTAATTTCTTTGATTTTCA SEQ ID NO:148	-17.5	-17.9	57.8	0.6	0	-2.7
329	GCTTGTGAACTTCTTCATCC SEQ ID NO:149	-17.4	-24	71.1	-5.7	-0.8	-5.2
1786	TTCTTTGATTTTCAGTGCCC SEQ ID NO:150	-17.4	-24.6	72.5	-7.2	0	-3.8
2251	AAAAAGGCTTCAAGGGGTGA SEQ ID NO:151	-17.4	-21	61.4	-3.1	-0.1	-7.6
157	TTCTCGTCTCGTTCGAGGAA SEQ ID NO:152	-17.3	-24.5	70.2	-4.7	-2.5	-9.1
490	GTAGTTGGTGATGATTCCAT SEQ ID NO:153	-17.3	-23	69.1	-5.1	-0.3	-3.9
533	CGAAGTCATAGCCTTTGCTT SEQ ID NO:154	-17.3	-24.4	69.8	-5.7	-1.3	-5.9
1043	GGAGTTCCATCTGGAGTGTT SEQ ID NO:155	-17.3	-25.8	77	-8.5	0.1	-6.6
1993	GTTCTTAATGGTCTCAGTAT SEQ ID NO:156	-17.3	-21.4	67.1	-4.1	0	-2.6
2192	GTTGCTTAATCATACAGTTT SEQ ID NO:157	-17.3	-20.2	62.7	-2.9	0	-3.6
326	TGTGAACTTCTTCATCCAGT SEQ ID NO:158	-17.2	-23.1	69.2	-4.5	-1.3	-4.2
857	CTTCCACCGGGAAAAGGCAG SEQ ID NO:159	-17.2	-25.7	68.9	-6.5	-2	-7.9
1135	GACTCTTCCTCTCATTGTGT SEQ ID NO:160	-17.2	-25.3	76.2	-8.1	0	-2.5
1527	GTACTGGCCACACCAATCTC SEQ ID NO:161	-17.2	-26.5	74.3	-8	-1.2	-8.4
1594	GATCCGATCATCACACATCA SEQ ID NO:162	-17.2	-23.5	67.3	-6.3	0	-6.8
2590	CCTTCCCTAACTGTCCAAGT SEQ ID NO:163	-17.2	-27.2	74.8	-9.4	-0.3	-3.2
1063	GTTGCCCTTCATGATCTGCT SEQ ID NO:164	-17.1	-27.8	78.9	-10.7	0	-6.8
1128	CCTCTCATTGTGTTCACGAC SEQ ID NO:165	-17.1	-24.8	71.9	-7.7	0	-6.4
1785	TCTTTGATTTTCAGTGCCCC SEQ ID NO:166	-17.1	-26.5	75.8	-9.4	0	-3.8
2254	TAAAAAAAGGCTTCAAGGGG SEQ ID NO:167	-17.1	-17.5	53.5	2.3	0	-3.7
324	TGAACTTCTTCATCCAGTGC SEQ ID NO:168	-17	-23.7	70.2	-5.7	-0.9	-5.3
386	GGGTATGAGCTATTCCAAGG SEQ ID NO:169	-17	-24	69.9	-6.5	-0.1	-5.1
403	TCCATGTGTTGCCCAACGGG SEQ ID NO:170	-17	-28.8	76.3	-10.8	-0.9	-7.7
530	AGTCATAGCCTTTGCTTTCC SEQ ID NO:171	-17	-26.2	76.8	-7.8	-1.3	-4.5

position	oligo	total binding	duplex formation	Tm of Duplex	target struc-ture	Intra-molec-ular oligo	Inter-Molec ular oligo
859	TTCTTCCACCGGGAAAAGGC SEQ ID NO:172	-17	-25.5	69.4	-6.5	-2	-7.1
1528	TGTACTGGCCACACCAATCT SEQ ID NO:173	-17	-26.1	72.5	-8	-1	-8.2
1787	TTTCTTTGATTTTCAGTGCC SEQ ID NO:174	-16.9	-22.7	69	-5.8	0	-3.8
2239	AGGGGTGATATTTTAAATCA SEQ ID NO:175	-16.9	-18.8	58.3	-1.4	-0.1	-4.7
2562	ACACTGCCACTGGCTTTAGA SEQ ID NO:176	-16.9	-26	73.8	-7.6	-1.4	-9
2854	AGCTTGAATTTAAAGTTTGT SEQ ID NO:177	-16.9	-17.8	56.4	-0.7	0	-4.9
22	CTGCGGGCTCGGGGGCCGGG SEQ ID NO:178	-16.8	-35.6	88.3	-16	-2.8	-11.8
1040	GTTCCATCTGGAGTGTTTGC SEQ ID NO:179	-16.8	-25.9	77.3	-8.6	-0.2	-6.9
1048	CTGCTGGAGTTCCATCTGGA SEQ ID NO:180	-16.8	-26.9	77.4	-9.5	-0.3	-6.5
2243	TTCAAGGGGTGATATTTTAA SEQ ID NO:181	-16.8	-18.9	58.7	-1.4	-0.3	-3.1
2255	CTAAAAAAAGGCTTCAAGGG SEQ ID NO:182	-16.8	-17.2	53	2.3	0	-3.7
33	CGGTGGGCAATCTGCGGGCT SEQ ID NO:183	-16.7	-30.4	80.1	-11.5	-2.2	-5.9
1641	AGCCGTTTCAATCCAAGCAT SEQ ID NO:184	-16.7	-25.3	70.1	-8.1	-0.2	-4.1
532	GAAGTCATAGCCTTTGCTTT SEQ ID NO:185	-16.6	-23.7	70.1	-5.7	-1.3	-5.9
1053	ATGATCTGCTGGAGTTCCAT SEQ ID NO:186	-16.6	-24.8	72.6	-7.6	-0.3	-6.3
1532	CCTTTGTACTGGCCACACCA SEQ ID NO:187	-16.6	-28.6	77.5	-10.8	-1.1	-8.4
2242	TCAAGGGGTGATATTTTAAA SEQ ID NO:188	-16.6	-18.1	56.4	-1.4	0	-4.2
396	GTTGCCCAACGGGTATGAGC SEQ ID NO:189	-16.5	-27.8	75.6	-10	-1.2	-7.1
408	GGTTCTCCATGTGTTGCCCA SEQ ID NO:190	-16.5	-29.9	83.6	-12.7	-0.4	-4.3
867	ACTGCTTTTTCTTCCACCGG SEQ ID NO:191	-16.5	-26.9	74.8	-10.4	0	-6.6
1050	ATCTGCTGGAGTTCCATCTG SEQ ID NO:192	-16.5	-25.5	75.1	-8.4	-0.3	-6.3
2191	TTGCTTAATCATACAGTTTC SEQ ID NO:193	-16.5	-19.4	60.9	-2.9	0	-3.6
2513	TGGTCTGAATGAAGTATGGT SEQ ID NO:194	-16.5	-20.8	63.3	-4.3	0	-3
2589	CTTCCCTAACTGTCCAAGTA SEQ ID NO:195	-16.5	-24.9	70.7	-7.7	-0.5	-3.2
93	ACACGGCCCGCGAGGCCAGG SEQ ID NO:196	-16.4	-33.8	82.7	-12.5	-4.7	-17.4
441	TCAGAGCGCTGGGGGTGGCT SEQ ID NO:197	-16.4	-30.9	85.4	-13.2	-1.2	-9.4
531	AAGTCATAGCCTTTGCTTTC SEQ ID NO:198	-16.4	-23.5	70.4	-5.7	-1.3	-5.5
545	CTGTTTCAGATTCGAAGTCA SEQ ID NO:199	-16.4	-21.5	65	-4.5	-0.1	-8.5
607	GGTATCTTGACTTTCCCGAT SEQ ID NO:200	-16.4	-25.2	71.6	-8.8	0	-2.8
1059	CCCTTCATGATCTGCTGGAG SEQ ID NO:201	-16.4	-26.5	74.9	-10.1	0	-6.4

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1318	CAGGAAGTCACTTGCTAGTT SEQ ID NO:202	-16.4	-23	69.3	-6.6	0	-1.7
1320	TCCAGGAAGTCACTTGCTAG SEQ ID NO:203	-16.4	-24.1	71	-7.7	0	-4.7
1589	GATCATCACACATCATAAGG SEQ ID NO:204	-16.4	-19.9	60.6	-3.5	0	-4.7
2193	TGTTGCTTAATCATACAGTT SEQ ID NO:205	-16.4	-20.1	62.2	-3.7	0	-3.6
384	GTATGAGCTATTCCAAGGTG SEQ ID NO:206	-16.3	-22.8	67.9	-6.5	0	-4.5
2200	TGTCTTGTGTTGCTTAATCA SEQ ID NO:207	-16.3	-22	67.5	-5.7	0	-3.6
2862	TCCAAAGCAGCTTGAATTTA SEQ ID NO:208	-16.3	-20.8	61.4	-3.9	0	-8.4
2870	GTCAGTTGTCCAAAGCAGCT SEQ ID NO:209	-16.3	-25.7	75	-8.8	-0.3	-6.1
395	TTGCCCAACGGGTATGAGCT SEQ ID NO:210	-16.2	-27.5	74.2	-10	-1.2	-7.5
410	TGGGTTCTCCATGTGTTGCC SEQ ID NO:211	-16.2	-28.4	81.5	-10.9	-1.2	-5
865	TGCTTTTTCTTCCACCGGGA SEQ ID NO:212	-16.2	-27.6	76.2	-10.4	-0.9	-7.1
1192	GATCTCCTTTATGTGATCCT SEQ ID NO:213	-16.2	-24.2	71.5	-7.3	-0.4	-4.4
2241	CAAGGGGTGATATTTTAAAT SEQ ID NO:215	-16.2	-17.7	55.1	-1.4	0	-4.5
84	GCGAGGCCAGGGGCGAGTGG SEQ ID NO:215	-16.1	-32.1	84.3	-14.3	-1.7	-7.7
156	TCTCGTCTCGTTCGAGGAAC SEQ ID NO:216	-16.1	-24.6	70.5	-6	-2.5	-9.1
327	TTGTGAACTTCTTCATCCAG SEQ ID NO:217	-16.1	-22	66.2	-4.5	-1.3	-5.1
1147	GTCATCAAAGTTGACTCTTC SEQ ID NO:218	-16.1	-20.8	64.6	-3.4	-1.2	-6
1196	TCTGGATCTCCTTTATGTGA SEQ ID NO:219	-16.1	-23.4	70.2	-7.3	0	-5.3
1317	AGGAAGTCACTTGCTAGTTC SEQ ID NO:220	-16.1	-22.7	69.8	-6.6	0	-1.7
1793	AAGTAATTTCTTTGATTTTC SEQ ID NO:221	-16.1	-16.5	54.4	0.6	0	-3.5
1981	CTCAGTATCCTCCTTATCAC SEQ ID NO:222	-16.1	-24.6	73	-8.5	0	-1.6
2588	TTCCCTAACTGTCCAAGTAT SEQ ID NO:223	-16.1	-24	68.8	-7.2	-0.5	-3.2
332	GTTGCTTGTGAACTTCTTCA SEQ ID NO:224	-16	-22.9	69.3	-5.7	-1.1	-5.8
333	TGTTGCTTGTGAACTTCTTC SEQ ID NO:225	-16	-22.2	67.9	-5.7	-0.1	-4.9
1529	TTGTACTGGCCACACCAATC SEQ ID NO:226	-16	-25.3	71	-8	-1.2	-8.4
1590	CGATCATCACACATCATAAG SEQ ID NO:227	-16	-19.5	58.7	-3.5	0	-4.9
1779	ATTTTCAGTGCCCCTTCAAG SEQ ID NO:228	-16	-25.8	73.2	-9.8	0	-3.2
398	GTGTTGCCCAACGGGTATGA SEQ ID NO:229	-15.9	-27.2	74.3	-10	-1.2	-7.7
2240	AAGGGGTGATATTTTAAATC SEQ ID NO:230	-15.9	-17.4	55.1	-1.4	0	-4.5
2668	AGTTTTACAGTTTGATTTAA SEQ ID NO:231	-15.9	-17.3	56.2	-1.3	0	-2.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
183	AGGCCTTTGATTAGGGTCTC SEQ ID NO:232	-15.8	-25.8	76.5	-9.3	-0.5	-7.9
529	GTCATAGCCTTTGCTTTCCA SEQ ID NO:233	-15.8	-26.9	77.6	-10	-1	-4.5
1977	GTATCCTCCTTATCACAAAT SEQ ID NO:234	-15.8	-21.9	64.5	-6.1	0	-1.9
1978	AGTATCCTCCTTATCACAAA SEQ ID NO:235	-15.8	-21.9	64.7	-6.1	0	-2.7
1994	TGTTCTTAATGGTCTCAGTA SEQ ID NO:236	-15.8	-21.4	66.9	-5.6	0	-2.6
2256	ACTAAAAAAAGGCTTCAAGG SEQ ID NO:237	-15.8	-16.2	51.2	2.3	0	-3.7
2523	ACTCTTTCACTGGTCTGAAT SEQ ID NO:238	-15.8	-22.4	67.8	-6.6	0	-3.6
182	GGCCTTTGATTAGGGTCTCC SEQ ID NO:239	-15.7	-27.8	79.9	-11.5	-0.3	-6.4
334	TTGTTGCTTGTGAACTTCTT SEQ ID NO:240	-15.7	-21.9	66.7	-5.7	-0.1	-4.9
418	GACAGGACTGGGTTCTCCAT SEQ ID NO:241	-15.7	-26.5	76.3	-9.5	-1.2	-6.9
419	TGACAGGACTGGGTTCTCCA SEQ ID NO:242	-15.7	-26.5	76.2	-9.5	-1.2	-6.9
1195	CTGGATCTCCTTTATGTGAT SEQ ID NO:243	-15.7	-23	68.5	-7.3	0	-5.3
2238	GGGGTGATATTTTAAATCAA SEQ ID NO:244	-15.7	-18.1	56.2	-1.4	-0.8	-5.4
8	GCCGGGGTGGCGCCGACACG SEQ ID NO:245	-15.6	-34.3	82.8	-16	-2.6	-12.6
486	TTGGTGATGATTCCATTGTG SEQ ID NO:246	-15.6	-22.2	66.2	-5.9	-0.5	-4.1
1058	CCTTCATGATCTGCTGGAGT SEQ ID NO:247	-15.6	-25.7	74.7	-10.1	0	-7.1
1304	CTAGTTCCACCATCACAGGC SEQ ID NO:248	-15.6	-26.9	76.5	-11.3	0	-3.7
1305	GCTAGTTCCACCATCACAGG SEQ ID NO:249	-15.6	-26.9	76.5	-11.3	0	-4.1
483	GTGATGATTCCATTGTGAAT SEQ ID NO:250	-15.5	-20.8	62.5	-4.6	-0.5	-6
720	GGGCTACCTCGCCTTGTGCC SEQ ID NO:251	-15.5	-32.9	87.1	-15.4	-2	-7.6
1074	AATGAACTGAAGTTGCCCTT SEQ ID NO:252	-15.5	-22.3	63.8	-6.8	0	-5.7
1583	CACACATCATAAGGGCAAAC SEQ ID NO:253	-15.5	-20.3	59.7	-4.8	0	-4
1642	CAGCCGTTTCAATCCAAGCA SEQ ID NO:254	-15.5	-26	71.2	-10	-0.2	-4.1
1789	AATTTCTTTGATTTTCAGTG SEQ ID NO:255	-15.5	-18.2	58.3	-2.7	0	-3.5
2876	CATATTGTCAGTTGTCCAAA SEQ ID NO:256	-15.5	-21	63.3	-5.5	0	-3.5
32	GGTGGGCAATCTGCGGGCTC SEQ ID NO:257	-15.4	-30	82.4	-13.1	-1.4	-6.9
390	CAACGGGTATGAGCTATTCC SEQ ID NO:258	-15.4	-23.8	67.8	-8.4	0	-5.2
548	TGTCTGTTTCAGATTCGAAG SEQ ID NO:259	-15.4	-20.8	63.7	-3.8	-1.4	-10.4
719	GGCTACCTCGCCTTGTGCCA SEQ ID NO:260	-15.4	-32.4	85.5	-15.4	-1.6	-7.1
722	GAGGGCTACCTCGCCTTGTG SEQ ID NO:261	-15.4	-29.7	81.1	-11.2	-3.1	-9.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1193	GGATCTCCTTTATGTGATCC SEQ ID NO:262	-15.4	-24.5	72.1	-7.3	-1.8	-6.2
1308	CTTGCTAGTTCCACCATCAC SEQ ID NO:263	-15.4	-26	74.6	-10.6	0	-4.1
2563	TACACTGCCACTGGCTTTAG SEQ ID NO:264	-15.4	-25.1	71.9	-7.6	-2.1	-9.7
2875	ATATTGTCAGTTGTCCAAAG SEQ ID NO:265	-15.4	-20.3	62.3	-4.9	0	-3.5
162	AGGATTTCTCGTCTCGTTCG SEQ ID NO:266	-15.3	-24.7	71.6	-8.9	-0.1	-4.1
606	GTATCTTGACTTTCCCGATT SEQ ID NO:267	-15.3	-24.1	69.4	-8.8	0	-2.8
860	TTTCTTCCACCGGGAAAAGG SEQ ID NO:268	-15.3	-23.8	65.9	-6.5	-2	-7.1
1794	TAAGTAATTTCTTTGATTTT SEQ ID NO:269	-15.3	-15.8	52.5	0.6	-0.2	-3.5
2210	ATACAAAAGGTGTCTTGTGT SEQ ID NO:270	-15.3	-19.9	61.3	-2.6	-2	-5.5
2262	GGATTTACTAAAAAAAGGCT SEQ ID NO:271	-15.3	-16.2	51.3	-0.7	0	-3.7
314	CATCCAGTGCCTTAACTTTT SEQ ID NO:272	-15.2	-24.2	69.6	-9	0	-3.6
402	CCATGTGTTGCCCAACGGGT SEQ ID NO:273	-15.2	-29.6	77.9	-13.1	-1.2	-7.7
413	GACTGGGTTCTCCATGTGTT SEQ ID NO:274	-15.2	-26.3	77.4	-9.8	-1.2	-4.7
557	TTGTCTCTGTGTCTGTTTCA SEQ ID NO:275	-15.2	-24.1	75.6	-8.9	0	-1.9
1524	CTGGCCACACCAATCTCAGG SEQ ID NO:276	-15.2	-27.3	74.8	-10.8	-1.2	-8.4
1795	ATAAGTAATTTCTTTGATTT SEQ ID NO:277	-15.2	-15.7	52.2	0.6	-0.2	-3.5
2209	TACAAAAGGTGTCTTGTGTT SEQ ID NO:278	-15.2	-20	61.6	-2.6	-2.2	-5.3
2259	TTTACTAAAAAAAGGCTTCA SEQ ID NO:279	-15.2	-15.6	50.4	2.3	0	-3.7
2515	ACTGGTCTGAATGAAGTATG SEQ ID NO:280	-15.2	-19.5	60	-4.3	0	-2.6
2561	CACTGCCACTGGCTTTAGAT SEQ ID NO:281	-15.2	-25.8	73.2	-8.5	-2.1	-9.7
2667	GTTTTACAGTTTGATTTAAA SEQ ID NO:282	-15.2	-16.6	54.1	-1.3	0	-4.6
319	TTCTTCATCCAGTGCCTTAA SEQ ID NO:283	-15.1	-24.7	71.9	-9.6	0	-3.6
417	ACAGGACTGGGTTCTCCATG SEQ ID NO:284	-15.1	-25.9	74.8	-9.5	-1.2	-6.9
491	TGTAGTTGGTGATGATTCCA SEQ ID NO:285	-15.1	-23	69	-7.3	-0.3	-3.7
556	TGTCTCTGTGTCTGTTTCAG SEQ ID NO:286	-15.1	-24	75.6	-8.9	0	-3.7
1073	ATGAACTGAAGTTGCCCTTC SEQ ID NO:287	-15.1	-23.4	67.3	-6.8	-1.4	-6.4
1998	TTTGTGTTCTTAATGGTCTC SEQ ID NO:288	-15.1	-21.2	66.7	-6.1	0	-2.3
2199	GTCTTGTGTTGCTTAATCAT SEQ ID NO:289	-15.1	-22	67.6	-6.9	0	-3.6
35	TTCGGTGGGCAATCTGCGGG SEQ ID NO:290	-15	-28.2	76.2	-11	-2.2	-6.6
99	CCGGAGACACGGCCCGCGAG SEQ ID NO:291	-15	-32.1	77.8	-15.9	-1.1	-9.2

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1041	AGTTCCATCTGGAGTGTTTG SEQ ID NO:292	-15	-24.1	72.9	-8.6	-0.2	-6.9
1148	AGTCATCAAAGTTGACTCTT SEQ ID NO:293	-15	-20.4	63.3	-3.4	-2	-6.5
1534	AGCCTTTGTACTGGCCACAC SEQ ID NO:294	-15	-27.7	77.5	-10.8	-1.9	-8.4
2190	TGCTTAATCATACAGTTTCG SEQ ID NO:295	-15	-20.1	61.1	-5.1	0	-3.6
2244	CTTCAAGGGGTGATATTTTA SEQ ID NO:296	-15	-20.5	62.7	-4.9	-0.3	-3.1
2522	CTCTTTCACTGGTCTGAATG SEQ ID NO:297	-15	-22.2	67.1	-6.6	-0.3	-3.6
313	ATCCAGTGCCTTAACTTTTC SEQ ID NO:298	-14.9	-23.9	70.1	-9	0	-3.6
330	TGCTTGTGAACTTCTTCATC SEQ ID NO:299	-14.9	-22	67.1	-5.7	-1.3	-6
389	AACGGGTATGAGCTATTCCA SEQ ID NO:300	-14.9	-23.8	67.8	-8.4	-0.1	-5.2
414	GGACTGGGTTCTCCATGTGT SEQ ID NO:301	-14.9	-27.4	79.8	-11.2	-1.2	-6.2
853	CACCGGGAAAAGGCAGGTTG SEQ ID NO:302	-14.9	-24.8	67.6	-9.4	-0.1	-7.1
1066	GAAGTTGCCCTTCATGATCT SEQ ID NO:303	-14.9	-25	71.8	-8.3	-1.8	-8.5
155	CTCGTCTCGTTCGAGGAACA SEQ ID NO:304	-14.8	-24.9	70	-8.2	-1.9	-8.8
397	TGTTGCCCAACGGGTATGAG SEQ ID NO:305	-14.8	-26	71.4	-10	-1.1	-7.7
420	TTGACAGGACTGGGTTCTCC SEQ ID NO:306	-14.8	-25.9	75.4	-10.6	-0.1	-5.9
449	TATTTTTATCAGAGCGCTGG SEQ ID NO:307	-14.8	-22	65.5	-5.9	-1.2	-9.4
1045	CTGGAGTTCCATCTGGAGTG SEQ ID NO:308	-14.8	-25.4	74.8	-10	-0.3	-6.9
1067	TGAAGTTGCCCTTCATGATC SEQ ID NO:309	-14.8	-24.1	69.7	-6.8	-2.5	-8.5
1072	TGAACTGAAGTTGCCCTTCA SEQ ID NO:310	-14.8	-24.1	68.5	-6.8	-2.5	-8.5
1526	TACTGGCCACACCAATCTCA SEQ ID NO:311	-14.8	-26	72.1	-9.9	-1.2	-8.4
1796	TATAAGTAATTTCTTTGATT SEQ ID NO:312	-14.8	-15.3	51.3	0.6	-0.2	-3.5
1999	TTTTGTGTTCTTAATGGTCT SEQ ID NO:313	-14.8	-20.9	65.4	-6.1	0	-2.3
2591	CCCTTCCCTAACTGTCCAAG SEQ ID NO:315	-14.8	-28	75	-13.2	0	-3.2
2934	GAAAACACAAAGTAGTAGGA SEQ ID NO:315	-14.8	-16.5	52.4	-1.7	0	-3
92	CACGGCCCGCGAGGCCAGGG SEQ ID NO:316	-14.7	-34.8	84.3	-15.2	-4.7	-17.4
248	CTTTATCATTGCCTCCATCA SEQ ID NO:317	-14.7	-24.9	71.7	-10.2	0	-3
435	CGCTGGGGGTGGCTATTGAC SEQ ID NO:318	-14.7	-28	77.6	-12.8	-0.2	-4.3
1071	GAACTGAAGTTGCCCTTCAT SEQ ID NO:319	-14.7	-24.1	68.6	-6.8	-2.6	-8.7
1075	AAATGAACTGAAGTTGCCCT SEQ ID NO:320	-14.7	-21.5	61.6	-6.8	0	-5.1
1321	GTCCAGGAAGTCACTTGCTA SEQ ID NO:321	-14.7	-25.3	74.2	-10.6	0	-5.5

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1523	TGGCCACACCAATCTCAGGA SEQ ID NO:322	-14.7	-27	74.3	-11.1	-1.1	-8.3
1797	ATATAAGTAATTTCTTTGAT SEQ ID NO:323	-14.7	-15.2	51	0.2	-0.2	-3.5
1976	TATCCTCCTTATCACAAATT SEQ ID NO:324	-14.7	-20.8	61.8	-6.1	0	-2.9
2877	TCATATTGTCAGTTGTCCAA SEQ ID NO:325	-14.7	-22.1	67.1	-7.4	0	-3.3
325	GTGAACTTCTTCATCCAGTG SEQ ID NO:326	-14.6	-23.1	69.2	-7.1	-1.3	-5.7
331	TTGCTTGTGAACTTCTTCAT SEQ ID NO:327	-14.6	-21.7	65.9	-5.7	-1.3	-6
387	CGGGTATGAGCTATTCCAAG SEQ ID NO:328	-14.6	-23.6	67.5	-8.5	-0.1	-5.2
1049	TCTGCTGGAGTTCCATCTGG SEQ ID NO:329	-14.6	-26.7	77.9	-11.6	-0.1	-6.1
2521	TCTTTCACTGGTCTGAATGA SEQ ID NO:330	-14.6	-21.9	66.4	-6.6	-0.5	-3.9
2565	CATACACTGCCACTGGCTTT SEQ ID NO:331	-14.6	-26.1	73.3	-9.4	-2.1	-9.7
2568	GAGCATACACTGCCACTGGC SEQ ID NO:332	-14.6	-27.4	76.5	-11.1	-1.7	-8.7
2932	AAACACAAAGTAGTAGGATA SEQ ID NO:333	-14.6	-16.3	52.4	-1.7	0	-3
317	CTTCATCCAGTGCCTTAACT SEQ ID NO:334	-14.5	-25.3	72.4	-10.8	0	-3.6
1582	ACACATCATAAGGGCAAACA SEQ ID NO:335	-14.5	-20.3	59.7	-5.8	0	-4
2001	CTTTTTGTGTTCTTAATGGT SEQ ID NO:336	-14.5	-20.6	64.2	-6.1	0	-2.3
2235	GTGATATTTTAAATCAAGGT SEQ ID NO:337	-14.5	-16.9	54.2	-1.4	-0.8	-5.4
2236	GGTGATATTTTAAATCAAGG SEQ ID NO:338	-14.5	-16.9	53.9	-1.4	-0.8	-5.4
2237	GGGTGATATTTTAAATCAAG SEQ ID NO:339	-14.5	-16.9	53.9	-1.4	-0.8	-5.4
2260	ATTTACTAAAAAAAGGCTTC SEQ ID NO:340	-14.5	-14.9	49.2	0.9	0	-3.7
2564	ATACACTGCCACTGGCTTTA SEQ ID NO:341	-14.5	-25.1	71.6	-8.5	-2.1	-9.7
207	TATCCTCTGTACTCCAGTCT SEQ ID NO:342	-14.4	-25.9	77.1	-10.6	-0.8	-4.8
328	CTTGTGAACTTCTTCATCCA SEQ ID NO:343	-14.4	-22.9	67.9	-7.1	-1.3	-4.2
555	GTCTCTGTGTCTGTTTCAGA SEQ ID NO:344	-14.4	-24.6	77.4	-8.9	-1.2	-6.1
631	TCTCTCCACCAAGGTAGTAA SEQ ID NO:345	-14.4	-24.2	70.5	-9.8	0.1	-5.1
852	ACCGGGAAAAGGCAGGTTGT SEQ ID NO:346	-14.4	-25.3	69.5	-10.9	0	-7.1
861	TTTTCTTCCACCGGGAAAAG SEQ ID NO:347	-14.4	-22.7	63.9	-6.5	-1.8	-7.8
921	ACGCGATTGGTGTGTTCTAT SEQ ID NO:348	-14.4	-24.2	69.7	-9.2	-0.2	-7.9
1149	TAGTCATCAAAGTTGACTCT SEQ ID NO:349	-14.4	-20	62.3	-3.4	-2.2	-7
1298	CCACCATCACAGGCAACTCA SEQ ID NO:350	-14.4	-26.8	73.3	-11.5	-0.8	-4.5
1306	TGCTAGTTCCACCATCACAG SEQ ID NO:351	-14.4	-25.7	73.7	-11.3	0	-4.1

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1995	GTGTTCTTAATGGTCTCAGT SEQ ID NO:352	-14.4	-22.9	71.3	-8.5	0	-2.4
2233	GATATTTTAAATCAAGGTTT SEQ ID NO:353	-14.4	-15.9	52.1	-1.4	0	-4.2
2258	TTACTAAAAAAAGGCTTCAA SEQ ID NO:354	-14.4	-14.8	48.6	2.3	0	-3.7
2263	AGGATTTACTAAAAAAAGGC SEQ ID NO:355	-14.4	-15.3	49.7	-0.7	0	-2.9
100	GCCGGAGACACGGCCCGCGA SEQ ID NO:356	-14.3	-33.9	81.1	-15.9	-3.4	-15.2
536	ATTCGAAGTCATAGCCTTTG SEQ ID NO:357	-14.3	-22.1	65.2	-7.8	0	-7.1
551	CTGTGTCTGTTTCAGATTCG SEQ ID NO:358	-14.3	-23	69.7	-7.7	-0.9	-5.9
862	TTTTTCTTCCACCGGGAAAA SEQ ID NO:359	-14.3	-22.8	64	-6.5	-2	-8
1042	GAGTTCCATCTGGAGTGTTT SEQ ID NO:360	-14.3	-24.7	74.6	-9.9	-0.2	-6.9
1194	TGGATCTCCTTTATGTGATC SEQ ID NO:361	-14.3	-22.5	68.1	-7.3	-0.8	-5.3
1323	CTGTCCAGGAAGTCACTTGC SEQ ID NO:362	-14.3	-25.6	74.6	-11.3	0	-5.5
1799	GCATATAAGTAATTTCTTTG SEQ ID NO:363	-14.3	-17.1	55	-2.3	-0.2	-3.6
2257	TACTAAAAAAAGGCTTCAAG SEQ ID NO:364	-14.3	-14.7	48.4	2.3	0	-3.7
2556	CCACTGGCTTTAGATACTCC SEQ ID NO:365	-14.3	-25.4	72.6	-11.1	0	-3.7
2878	ATCATATTGTCAGTTGTCCA SEQ ID NO:366	-14.3	-22.8	69.5	-8.5	0	-2.1
494	CTTTGTAGTTGGTGATGATT SEQ ID NO:367	-14.2	-21	65	-6.8	0	-1.8
544	TGTTTCAGATTCGAAGTCAT SEQ ID NO:368	-14.2	-20.6	63	-5.9	-0.1	-7.6
806	TTCCTTTCTTGTCTTTGCCT SEQ ID NO:369	-14.2	-26.4	77.6	-12.2	0	-3
807	CTTCCTTTCTTGTCTTTGCC SEQ ID NO:370	-14.2	-26.4	77.6	-12.2	0	-3
1054	CATGATCTGCTGGAGTTCCA SEQ ID NO:371	-14.2	-25.5	73.8	-10.8	-0.2	-6.1
1773	AGTGCCCCTTCAAGACAAGT SEQ ID NO:372	-14.2	-26.4	73.6	-12.2	0	-3
1778	TTTTCAGTGCCCCTTCAAGA SEQ ID NO:373	-14.2	-26.4	74.5	-12.2	0	-3.8
1906	CTTGGCATAAGTGTGATCTC SEQ ID NO:374	-14.2	-22.4	67.8	-8.2	0	-6.5
2853	GCTTGAATTTAAAGTTTGTG SEQ ID NO:375	-14.2	-17.8	56.2	-3.6	0	-4.9
2933	AAAACACAAAGTAGTAGGAT SEQ ID NO:376	-14.2	-15.9	51.2	-1.7	0	-3
2935	TGAAAACACAAAGTAGTAGG SEQ ID NO:377	-14.2	-15.9	51.2	-1.7	0	-3
247	TTTATCATTGCCTCCATCAA SEQ ID NO:378	-14.1	-23.3	67.5	-9.2	0	-3
376	TATTCCAAGGTGTACATCAA SEQ ID NO:379	-14.1	-20.8	62.5	-6.2	0	-7.9
724	CAGAGGGCTACCTCGCCTTG SEQ ID NO:380	-14.1	-29.2	79.1	-11.2	-3.9	-9.6
1197	CTCTGGATCTCCTTTATGTG SEQ ID NO:381	-14.1	-23.7	70.9	-9.6	0	-5.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1535	AAGCCTTTGTACTGGCCACA SEQ ID NO:382	-14.1	-26.8	74.5	-10.8	-1.9	-8.4
1980	TCAGTATCCTCCTTATCACA SEQ ID NO:383	-14.1	-24.4	72.2	-10.3	0	-2.7
2211	AATACAAAAGGTGTCTTGTG SEQ ID NO:384	-14.1	-18	56.2	-2.6	-1.2	-5.7
3050	TTTAATAGCAGCTCTGTGTT SEQ ID NO:385	-14.1	-21.9	67.1	-7.8	0	-6.1
453	TCATTATTTTTATCAGAGCG SEQ ID NO:386	-14	-19.3	59.8	-5.3	0	-4.1
539	CAGATTCGAAGTCATAGCCT SEQ ID NO:387	-14	-23.2	67.3	-8.7	-0.1	-7.6
1640	GCCGTTTCAATCCAAGCATG SEQ ID NO:388	-14	-25.3	69.7	-11.3	0	-4.3
2000	TTTTTGTGTTCTTAATGGTC SEQ ID NO:389	-14	-20.1	63.6	-6.1	0	-2.3
2212	AAATACAAAAGGTGTCTTGT SEQ ID NO:390	-14	-17.3	54.5	-2.6	-0.4	-5.5
2261	GATTTACTAAAAAAAGGCTT SEQ ID NO:391	-14	-15.1	49.3	-1	0	-3.7
2669	AAGTTTTACAGTTTGATTTA SEQ ID NO:392	-14	-17.3	56.2	-3.3	0	-2.6
3049	TTAATAGCAGCTCTGTGTTG SEQ ID NO:393	-14	-21.8	66.6	-7.8	0	-5.8
3051	ATTTAATAGCAGCTCTGTGT SEQ ID NO:394	-14	-21.8	66.7	-7.8	0	-6.1
180	CCTTTGATTAGGGTCTCCAG SEQ ID NO:395	-13.9	-25.5	74.1	-10.4	-1.1	-4.1
184	AAGGCCTTTGATTAGGGTCT SEQ ID NO:396	-13.9	-24.7	72.1	-9.3	-0.7	-10.9
558	ATTGTCTCTGTGTCTGTTTC SEQ ID NO:397	-13.9	-23.4	74.3	-9.5	0	-0.6
821	GAGAGAGATTGCAGCTTCCT SEQ ID NO:398	-13.9	-25.1	73.7	-11.2	0	-5.3
1191	ATCTCCTTTATGTGATCCTT SEQ ID NO:399	-13.9	-23.7	70.5	-9.8	0	-4.3
1772	GTGCCCCTTCAAGACAAGTA SEQ ID NO:400	-13.9	-26.1	72.8	-12.2	0	-3
2066	ACTGTAAAGGGATCACGCTG SEQ ID NO:401	-13.9	-22.4	64.6	-7.1	-1.3	-6.6
2189	GCTTAATCATACAGTTTCGT SEQ ID NO:402	-13.9	-21.3	64.3	-7.4	0	-3
2232	ATATTTTAAATCAAGGTTTT SEQ ID NO:403	-13.9	-15.4	51.1	-1.4	0	-4.5
2579	TGTCCAAGTATGAGCATACA SEQ ID NO:404	-13.9	-22.2	65.9	-6.8	-1.4	-9.6
2938	AGATGAAAACACAAAGTAGT SEQ ID NO:405	-13.9	-15.6	50.6	-1.7	0	-2.9
29	GGGCAATCTGCGGGCTCGGG SEQ ID NO:406	-13.8	-30.8	81.1	-14.8	-2.2	-8.4
1091	ATATTTCCTTCTGCATAAAT SEQ ID NO:407	-13.8	-19.4	59.2	-5.6	0	-4.9
1530	TTTGTACTGGCCACACCAAT SEQ ID NO:408	-13.8	-25	69.8	-9.9	-1.2	-8.4
2005	CGTTCTTTTTGTGTTCTTAA SEQ ID NO:409	-13.8	-20.7	63.9	-6.9	0	-2
2874	TATTGTCAGTTGTCCAAAGC SEQ ID NO:410	-13.8	-22.1	66.6	-8.3	0	-3.5
316	TTCATCCAGTGCCTTAACTT SEQ ID NO:411	-13.7	-24.5	70.9	-10.8	0	-3.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
374	TTCCAAGGTGTACATCAAAT SEQ ID NO:412	-13.7	-20.4	61	-6.2	0	-7.9
375	ATTCCAAGGTGTACATCAAA SEQ ID NO:413	-13.7	-20.4	61	-6.2	0	-7.9
549	GTGTCTGTTTCAGATTCGAA SEQ ID NO:415	-13.7	-22	66.8	-6.7	-1.4	-10.2
804	CCTTTCTTGTCTTTGCCTGT SEQ ID NO:415	-13.7	-27.1	78.8	-13.4	0	-3
920	CGCGATTGGTGTGTTCTATG SEQ ID NO:416	-13.7	-24	69	-10.3	0	-6.4
1046	GCTGGAGTTCCATCTGGAGT SEQ ID NO:417	-13.7	-27.2	79.6	-12.9	-0.3	-6.9
1057	CTTCATGATCTGCTGGAGTT SEQ ID NO:418	-13.7	-23.8	71.3	-10.1	0	-7.1
1069	ACTGAAGTTGCCCTTCATGA SEQ ID NO:419	-13.7	-24.8	70.7	-8.5	-2.6	-8.7
1774	CAGTGCCCCTTCAAGACAAG SEQ ID NO:420	-13.7	-25.9	71.4	-12.2	0	-3
2002	TCTTTTTGTGTTCTTAATGG SEQ ID NO:421	-13.7	-19.8	62.4	-6.1	0	-2.3
2234	TGATATTTTAAATCAAGGTT SEQ ID NO:422	-13.7	-15.8	51.7	-1.4	-0.4	-4.7
2524	TACTCTTTCACTGGTCTGAA SEQ ID NO:423	-13.7	-22.1	67.2	-7.9	-0.1	-3.5
2855	CAGCTTGAATTTAAAGTTTG SEQ ID NO:424	-13.7	-17.3	54.8	-3.6	0	-4.9
1127	CTCTCATTGTGTTCACGACA SEQ ID NO:425	-13.6	-23.5	69.4	-9.2	-0.5	-6.4
1307	TTGCTAGTTCCACCATCACA SEQ ID NO:426	-13.6	-25.8	73.8	-12.2	0	-4.1
1956	ACCACAGGCCGCCCCTGCCG SEQ ID NO:427	-13.6	-36.9	87.5	-20.5	-2.8	-8.7
2231	TATTTTAAATCAAGGTTTTA SEQ ID NO:428	-13.6	-15.1	50.5	-1.4	0	-4.5
2343	ACAAATTACTGGGAAAATGT SEQ ID NO:429	-13.6	-16.5	51.9	-2.9	0	-3.2
2937	GATGAAAACACAAAGTAGTA SEQ ID NO:430	-13.6	-15.3	49.9	-1.7	0	-3
540	TCAGATTCGAAGTCATAGCC SEQ ID NO:431	-13.5	-22.7	66.9	-8.7	-0.1	-7.6
634	AACTCTCTCCACCAAGGTAG SEQ ID NO:432	-13.5	-24.4	70.3	-10.4	-0.2	-5.1
721	AGGGCTACCTCGCCTTGTGC SEQ ID NO:433	-13.5	-30.9	84.1	-15.4	-2	-7.3
819	GAGAGATTGCAGCTTCCTTT SEQ ID NO:434	-13.5	-24.7	72.7	-11.2	0	-5.3
1055	TCATGATCTGCTGGAGTTCC SEQ ID NO:435	-13.5	-25.2	74.4	-11.7	0	-6.9
1076	TAAATGAACTGAAGTTGCCC SEQ ID NO:436	-13.5	-20.3	59.3	-6.8	0	-5.7
1150	ATAGTCATCAAAGTTGACTC SEQ ID NO:437	-13.5	-19.1	60.3	-3.4	-2.2	-7
2009	TGATCGTTCTTTTTGTGTTC SEQ ID NO:438	-13.5	-21.7	67.2	-8.2	0	-5.3
2065	CTGTAAAGGGATCACGCTGA SEQ ID NO:439	-13.5	-22.8	65.4	-8.6	-0.4	-6.4
175	GATTAGGGTCTCCAGGATTT SEQ ID NO:440	-13.4	-24.4	72.5	-10.4	-0.3	-5
206	ATCCTCTGTACTCCAGTCTC SEQ ID NO:441	-13.4	-26.6	79.7	-12.7	-0.2	-4.8

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
311	CCAGTGCCTTAACTTTTCCT SEQ ID NO:442	-13.4	-26.4	74	-13	0	-3.6
391	CCAACGGGTATGAGCTATTC SEQ ID NO:443	-13.4	-23.8	67.8	-10.4	0	-5.2
407	GTTCTCCATGTGTTGCCCAA SEQ ID NO:444	-13.4	-28	78.3	-14.6	0	-4.3
552	TCTGTGTCTGTTTCAGATTC SEQ ID NO:445	-13.4	-22.6	71.5	-7.7	-1.4	-6.3
603	TCTTGACTTTCCCGATTGTC SEQ ID NO:446	-13.4	-24.8	71.5	-11.4	0	-3.9
820	AGAGAGATTGCAGCTTCCTT SEQ ID NO:447	-13.4	-24.6	72.6	-11.2	0	-5.3
1014	CGTCCGGGGTGATCTCCTGC SEQ ID NO:448	-13.4	-31	83.1	-17	-0.3	-6.6
1303	TAGTTCCACCATCACAGGCA SEQ ID NO:449	-13.4	-26.7	75.6	-13.3	0	-4
1322	TGTCCAGGAAGTCACTTGCT SEQ ID NO:450	-13.4	-25.6	74.6	-12.2	0	-5.5
1769	CCCCTTCAAGACAAGTAGCA SEQ ID NO:451	-13.4	-25.6	71	-12.2	0	-4.1
1905	TTGGCATAAGTGTGATCTCT SEQ ID NO:452	-13.4	-22.4	67.8	-9	0	-6.5
1957	TACCACAGGCCGCCCCTGCC SEQ ID NO:453	-13.4	-35.8	87.7	-20.5	-1.9	-7.8
2512	GGTCTGAATGAAGTATGGTG SEQ ID NO:454	-13.4	-20.8	63.3	-7.4	0	-3
3061	ATCAATATTAATTTAATAGC SEQ ID NO:455	-13.4	-13.9	47.7	-0.2	0.1	-6.6
101	TGCCGGAGACACGGCCCGCG SEQ ID NO:456	-13.3	-33.3	79.8	-15.9	-4.1	-14.4
335	CTTGTTGCTTGTGAACTTCT SEQ ID NO:457	-13.3	-22.7	68.3	-8.9	-0.1	-4.9
454	TTCATTATTTTTATCAGAGC SEQ ID NO:458	-13.3	-18.6	59.6	-5.3	0	-2.8
971	AAAGACGTCCATCCACTACT SEQ ID NO:459	-13.3	-23.5	66.2	-9.6	0	-8.6
2218	GGTTTTAAATACAAAAGGTG SEQ ID NO:460	-13.3	-15.9	51.3	-2.6	0	-5.4
2219	AGGTTTTAAATACAAAAGGT SEQ ID NO:461	-13.3	-15.9	51.4	-2.6	0	-5.4
2525	CTACTCTTTCACTGGTCTGA SEQ ID NO:462	-13.3	-23.7	71.7	-10.4	0	-2.8
2560	ACTGCCACTGGCTTTAGATA SEQ ID NO:463	-13.3	-24.8	71.5	-9.4	-2.1	-9.7
2666	TTTTACAGTTTGATTTAAAA SEQ ID NO:464	-13.3	-14.7	49.5	-1.3	0	-5.2
168	GTCTCCAGGATTTCTCGTCT SEQ ID NO:465	-13.2	-26.6	78.6	-12.9	-0.1	-5
415	AGGACTGGGTTCTCCATGTG SEQ ID NO:466	-13.2	-26.2	76.4	-11.7	-1.2	-6.1
635	TAACTCTCTCCACCAAGGTA SEQ ID NO:467	-13.2	-24.1	69.5	-10.4	-0.2	-5.1
1011	CCGGGGTGATCTCCTGCAGT SEQ ID NO:468	-13.2	-30.5	83.2	-16.3	-0.8	-8.9
1065	AAGTTGCCCTTCATGATCTG SEQ ID NO:469	-13.2	-24.4	70.3	-11.2	0	-6.4
1089	ATTTCCTTCTGCATAAATGA SEQ ID NO:470	-13.2	-20.3	61	-7.1	0	-4.9
1746	TGATAGCCTCGTCCCATTAT SEQ ID NO:471	-13.2	-26.3	73.1	-13.1	0	-3.1

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1747	ATGATAGCCTCGTCCCATTA SEQ ID NO:472	-13.2	-26.3	73.1	-13.1	0	-3.2
1798	CATATAAGTAATTTCTTTGA SEQ ID NO:473	-13.2	-15.9	52.3	-2.7	0.1	-3.1
2310	ACAAAAATCACATATTGAGT SEQ ID NO:474	-13.2	-15.7	50.8	-1.9	-0.3	-4.5
2566	GCATACACTGCCACTGGCTT SEQ ID NO:475	-13.2	-27.8	77.1	-12.5	-2.1	-9.7
2670	TAAGTTTTACAGTTTGATTT SEQ ID NO:476	-13.2	-17.3	56.2	-4.1	0	-2.6
2857	AGCAGCTTGAATTTAAAGTT SEQ ID NO:477	-13.2	-19	58.7	-5.8	0	-5.6
2922	TAGTAGGATACCCAACATGT SEQ ID NO:478	-13.2	-22.4	65.4	-8.3	-0.8	-7.9
164	CCAGGATTTCTCGTCTCGTT SEQ ID NO:479	-13.1	-26.2	74.8	-12.6	-0.1	-3.5
179	CTTTGATTAGGGTCTCCAGG SEQ ID NO:480	-13.1	-24.7	73	-10.4	-1.1	-4.4
208	ATATCCTCTGTACTCCAGTC SEQ ID NO:481	-13.1	-25	74.9	-11	-0.8	-4.8
868	CACTGCTTTTTCTTCCACCG SEQ ID NO:482	-13.1	-26.4	73.4	-13.3	0	-3.6
1199	ATCTCTGGATCTCCTTTATG SEQ ID NO:483	-13.1	-22.9	69.2	-9.8	0	-5.3
1451	CTGTGTTTGTGATCCCCACA SEQ ID NO:484	-13.1	-27.3	76.5	-12.3	-1.9	-6.3
1536	TAAGCCTTTGTACTGGCCAC SEQ ID NO:485	-13.1	-25.8	72.8	-10.8	-1.9	-8.4
1581	CACATCATAAGGGCAAACAT SEQ ID NO:486	-13.1	-20.1	59.2	-7	0	-4
1768	CCCTTCAAGACAAGTAGCAT SEQ ID NO:487	-13.1	-23.6	67.5	-10.5	0	-4.1
2342	CAAATTACTGGGAAAATGTA SEQ ID NO:488	-13.1	-16	50.9	-2.9	0	-3.2
163	CAGGATTTCTCGTCTCGTTC SEQ ID NO:489	-13	-24.6	72.8	-11.1	-0.1	-3.5
495	TCTTTGTAGTTGGTGATGAT SEQ ID NO:490	-13	-21.3	66.2	-8.3	0	-2
598	ACTTTCCCGATTGTCATACA SEQ ID NO:491	-13	-24.1	68.7	-11.1	0	-4.4
602	CTTGACTTTCCCGATTGTCA SEQ ID NO:492	-13	-25.1	71	-11	-1	-5.3
972	GAAAGACGTCCATCCACTAC SEQ ID NO:493	-13	-23.2	65.6	-9.6	0	-8.6
1013	GTCCGGGGTGATCTCCTGCA SEQ ID NO:494	-13	-30.9	84.7	-17	-0.8	-6.6
1151	TATAGTCATCAAAGTTGACT SEQ ID NO:495	-13	-18.4	58.2	-3.4	-2	-6.6
1330	TGTGTTTCTGTCCAGGAAGT SEQ ID NO:496	-13	-24.5	73.6	-11.5	0.2	-5.5
1522	GGCCACACCAATCTCAGGAC SEQ ID NO:497	-13	-27.2	75	-13.5	-0.4	-7
1907	ACTTGGCATAAGTGTGATCT SEQ ID NO:498	-13	-22.2	66.8	-8.2	-0.9	-6.9
1975	ATCCTCCTTATCACAAATTA SEQ ID NO:499	-13	-20.8	61.8	-7.8	0	-3.2
2004	GTTCTTTTTGTGTTCTTAAT SEQ ID NO:500	-13	-19.9	63.4	-6.9	0	-2.3
2068	CAACTGTAAAGGGATCACGC SEQ ID NO:501	-13	-21.5	62	-7.1	-1.3	-6.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2069	GCAACTGTAAAGGGATCACG SEQ ID NO:502	-13	-21.5	62	-7.1	-1.3	-6.6
2194	GTGTTGCTTAATCATACAGT SEQ ID NO:503	-13	-21.2	65.2	-8.2	0	-1.3
2309	CAAAAATCACATATTGAGTG SEQ ID NO:504	-13	-15.5	50.3	-1.9	-0.3	-4.5
2555	CACTGGCTTTAGATACTCCA SEQ ID NO:505	-13	-24.1	70.1	-11.1	0	-3.3
2936	ATGAAAACACAAAGTAGTAG SEQ ID NO:506	-13	-14.7	48.8	-1.7	0	-3
23	TCTGCGGGCTCGGGGGCCGG SEQ ID NO:507	-12.9	-34.8	87.7	-18.3	-3.6	-11.8
25	AATCTGCGGGCTCGGGGGCC SEQ ID NO:508	-12.9	-32.1	83.4	-16.7	-2.5	-11.4
154	TCGTCTCGTTCGAGGAACAT SEQ ID NO:509	-12.9	-24	68.1	-9.2	-1.9	-9.1
181	GCCTTTGATTAGGGTCTCCA SEQ ID NO:510	-12.9	-27.3	78.3	-13.2	-1.1	-4.7
239	TGCCTCCATCAAATCCCACA SEQ ID NO:511	-12.9	-27.5	73.3	-14.6	0	-3
373	TCCAAGGTGTACATCAAATT SEQ ID NO:512	-12.9	-20.4	61	-7.5	0	-7.1
379	AGCTATTCCAAGGTGTACAT SEQ ID NO:513	-12.9	-23.1	68.4	-10.2	0	-6.6
392	CCCAACGGGTATGAGCTATT SEQ ID NO:515	-12.9	-25.4	69.8	-11.8	-0.5	-6.1
869	CCACTGCTTTTTCTTCCACC SEQ ID NO:515	-12.9	-27.6	77.1	-14.7	0	-2.9
1095	TCAAATATTTCCTTCTGCAT SEQ ID NO:516	-12.9	-20.8	62.4	-7.9	0	-6
1525	ACTGGCCACACCAATCTCAG SEQ ID NO:517	-12.9	-26.3	72.9	-12.1	-1.2	-8.4
1537	ATAAGCCTTTGTACTGGCCA SEQ ID NO:518	-12.9	-25.6	72.2	-10.8	-1.9	-8.3
1595	AGATCCGATCATCACACATC SEQ ID NO:519	-12.9	-22.8	66.4	-9	-0.7	-7.5
1745	GATAGCCTCGTCCCATTATC SEQ ID NO:520	-12.9	-26.7	74.9	-13.8	0	-3.2
2196	TTGTGTTGCTTAATCATACA SEQ ID NO:521	-12.9	-20.1	61.9	-7.2	0	-1.2
166	CTCCAGGATTTCTCGTCTCG SEQ ID NO:522	-12.8	-26.2	74.7	-12.9	-0.1	-5
169	GGTCTCCAGGATTTCTCGTC SEQ ID NO:523	-12.8	-26.9	79.3	-13.6	-0.1	-5
178	TTTGATTAGGGTCTCCAGGA SEQ ID NO:524	-12.8	-24.4	72.4	-10.4	-1.1	-5.3
315	TCATCCAGTGCCTTAACTTT SEQ ID NO:525	-12.8	-24.5	70.9	-11.7	0	-3.1
478	GATTCCATTGTGAATAACGA SEQ ID NO:526	-12.8	-19.6	58.2	-6.1	-0.5	-6.1
550	TGTGTCTGTTTCAGATTCGA SEQ ID NO:527	-12.8	-22.7	69	-8.1	-1.4	-11.3
626	CCACCAAGGTAGTAAAGCTG SEQ ID NO:528	-12.8	-23.2	66.1	-10.4	0	-5.1
630	CTCTCCACCAAGGTAGTAAA SEQ ID NO:529	-12.8	-23.1	66.7	-9.8	-0.2	-5.1
718	GCTACCTCGCCTTGTGCCAA SEQ ID NO:530	-12.8	-30.5	80.5	-17.1	-0.3	-4.4
919	GCGATTGGTGTGTTCTATGA SEQ ID NO:531	-12.8	-23.8	70.2	-11	0	-3.4

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1748	AATGATAGCCTCGTCCCATT SEQ ID NO:532	-12.8	-25.9	71.3	-13.1	0	-3.3
1896	GTGTGATCTCTCATGATGAT SEQ ID NO:533	-12.8	-21.9	67.2	-8.4	-0.4	-6.9
1897	AGTGTGATCTCTCATGATGA SEQ ID NO:534	-12.8	-21.9	67.5	-8.4	-0.4	-6.2
2217	GTTTTAAATACAAAAGGTGT SEQ ID NO:535	-12.8	-15.9	51.5	-2.6	-0.2	-5.8
2230	ATTTTAAATCAAGGTTTTAA SEQ ID NO:536	-12.8	-14.7	49.4	-1.4	-0.1	-4.5
2516	CACTGGTCTGAATGAAGTAT SEQ ID NO:537	-12.8	-20.2	61.4	-7.4	0	-3
2569	TGAGCATACACTGCCACTGG SEQ ID NO:538	-12.8	-25.6	72.1	-11.1	-1.7	-5.1
2577	TCCAAGTATGAGCATACACT SEQ ID NO:539	-12.8	-22.1	65.3	-8.4	-0.6	-8.8
2927	CAAAGTAGTAGGATACCCAA SEQ ID NO:540	-12.8	-20.8	61.1	-6.9	-1	-4.1
2931	AACACAAAGTAGTAGGATAC SEQ ID NO:541	-12.8	-17.2	54.7	-3.7	-0.4	-3.6
176	TGATTAGGGTCTCCAGGATT SEQ ID NO:542	-12.7	-24.3	72	-10.4	-1.1	-5.4
177	TTGATTAGGGTCTCCAGGAT SEQ ID NO:543	-12.7	-24.3	72	-10.4	-1.1	-5.4
210	TCATATCCTCTGTACTCCAG SEQ ID NO:544	-12.7	-24.5	72.5	-11.1	-0.5	-4.8
240	TTGCCTCCATCAAATCCCAC SEQ ID NO:545	-12.7	-26.9	72.7	-14.2	0	-3
380	GAGCTATTCCAAGGTGTACA SEQ ID NO:546	-12.7	-23.7	69.8	-11	0	-6.4
429	GGGTGGCTATTGACAGGACT SEQ ID NO:547	-12.7	-25.7	74.4	-13	0	-3
482	TGATGATTCCATTGTGAATA SEQ ID NO:548	-12.7	-19.3	58.9	-5.9	-0.5	-5.5
528	TCATAGCCTTTGCTTTCCAA SEQ ID NO:549	-12.7	-25	71.6	-10.9	-1.3	-4.3
627	TCCACCAAGGTAGTAAAGCT SEQ ID NO:550	-12.7	-23.6	67.7	-10.4	-0.2	-5.2
632	CTCTCTCCACCAAGGTAGTA SEQ ID NO:551	-12.7	-25.8	75	-12.6	-0.2	-5.1
1009	GGGGTGATCTCCTGCAGTTC SEQ ID NO:552	-12.7	-28.2	82.6	-14.7	-0.3	-8.9
1086	TCCTTCTGCATAAATGAACT SEQ ID NO:553	-12.7	-20.5	60.8	-7.8	0	-4.9
1877	TCATGATCACAGGCATCAAT SEQ ID NO:554	-12.7	-21.8	64.7	-8.4	-0.4	-6.8
1878	ATCATGATCACAGGCATCAA SEQ ID NO:555	-12.7	-21.8	64.7	-8.4	-0.4	-7.7
1879	GATCATGATCACAGGCATCA SEQ ID NO:556	-12.7	-23.1	68.3	-8.4	0.1	-12.1
2197	CTTGTGTTGCTTAATCATAC SEQ ID NO:557	-12.7	-20.3	62.7	-7.6	0	-3.6
2592	ACCCTTCCCTAACTGTCCAA SEQ ID NO:558	-12.7	-28.2	75.2	-15.5	0	-3.2
5	GGGGTGGCGCCGACACGACT SEQ ID NO:559	-12.6	-31.4	79.8	-16.7	-1.6	-12.1
30	TGGGCAATCTGCGGGCTCGG SEQ ID NO:560	-12.6	-29.6	78.5	-14.8	-2.2	-8.4
493	TTTGTAGTTGGTGATGATTC SEQ ID NO:561	-12.6	-20.5	64.5	-7.9	0	-1.8

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
604	ATCTTGACTTTCCCGATTGT SEQ ID NO:562	-12.6	-24.4	69.8	-11.8	0	-2.8
636	ATAACTCTCTCCACCAAGGT SEQ ID NO:563	-12.6	-24.4	70	-11.3	-0.2	-4.7
1062	TTGCCCTTCATGATCTGCTG SEQ ID NO:564	-12.6	-26.6	75.2	-14	0	-6.8
1087	TTCCTTCTGCATAAATGAAC SEQ ID NO:565	-12.6	-19.7	59.3	-7.1	0	-4.9
2214	TTAAATACAAAAGGTGTCTT SEQ ID NO:566	-12.6	-15.9	51.5	-2.6	-0.4	-3.3
2215	TTTAAATACAAAAGGTGTCT SEQ ID NO:567	-12.6	-15.9	51.5	-2.6	-0.4	-6.4
2557	GCCACTGGCTTTAGATACTC SEQ ID NO:568	-12.6	-25.2	73.3	-11.1	-1.4	-8.9
83	CGAGGCCAGGGGCGAGTGGC SEQ ID NO:569	-12.5	-32.1	84.3	-17.1	-2.5	-8.9
102	ATGCCGGAGACACGGCCCGC SEQ ID NO:570	-12.5	-32.5	80.2	-15.9	-4.1	-11.2
388	ACGGGTATGAGCTATTCCAA SEQ ID NO:571	-12.5	-23.8	67.8	-10.8	-0.1	-5.2
434	GCTGGGGGTGGCTATTGACA SEQ ID NO:572	-12.5	-27.9	79	-15.4	0	-3.7
543	GTTTCAGATTCGAAGTCATA SEQ ID NO:573	-12.5	-20.3	62.5	-7.3	-0.1	-7.6
863	CTTTTTCTTCCACCGGGAAA SEQ ID NO:574	-12.5	-24.4	67.8	-9.9	-2	-7.1
1010	CGGGGTGATCTCCTGCAGTT SEQ ID NO:575	-12.5	-28.6	80.1	-15.1	-0.8	-8.9
1039	TTCCATCTGGAGTGTTTGCA SEQ ID NO:576	-12.5	-25.4	74.8	-11.5	-0.2	-10.7
1088	TTTCCTTCTGCATAAATGAA SEQ ID NO:577	-12.5	-19.6	59.1	-7.1	0	-4.9
1096	CTCAAATATTTCCTTCTGCA SEQ ID NO:578	-12.5	-21.7	64.3	-9.2	0	-6
1296	ACCATCACAGGCAACTCAGT SEQ ID NO:579	-12.5	-25.3	72.3	-11.9	-0.8	-4.5
1331	GTGTGTTTCTGTCCAGGAAG SEQ ID NO:580	-12.5	-24.5	73.6	-11.5	-0.1	-5.5
1531	CTTTGTACTGGCCACACCAA SEQ ID NO:581	-12.5	-25.9	71.7	-12.1	-1.2	-8.4
1974	TCCTCCTTATCACAAATTAC SEQ ID NO:582	-12.5	-21	62.3	-8.5	0	-3.2
2213	TAAATACAAAAGGTGTCTTG SEQ ID NO:583	-12.5	-15.8	51.2	-2.6	-0.4	-4.8
2578	GTCCAAGTATGAGCATACAC SEQ ID NO:584	-12.5	-22.4	66.6	-8.4	-1.4	-9.6
2665	TTTACAGTTTGATTTAAAAA SEQ ID NO:585	-12.5	-13.9	47.6	-1.3	0	-5.2
3060	TCAATATTAATTTAATAGCA SEQ ID NO:586	-12.5	-14.6	49	-1.4	-0.4	-7.1
7	CCGGGGTGGCGCCGACACGA SEQ ID NO:587	-12.4	-33.1	80.2	-18.3	-1.7	-12.8
165	TCCAGGATTTCTCGTCTCGT SEQ ID NO:588	-12.4	-26.5	76.2	-14.1	0.3	-4.7
167	TCTCCAGGATTTCTCGTCTC SEQ ID NO:589	-12.4	-25.8	76.7	-12.9	-0.1	-5
318	TCTTCATCCAGTGCCTTAAC SEQ ID NO:590	-12.4	-24.8	72.1	-12.4	0	-3.6
537	GATTCGAAGTCATAGCCTTT SEQ ID NO:591	-12.4	-22.7	66.6	-10.3	0	-7.1

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1324	TCTGTCCAGGAAGTCACTTG SEQ ID NO:592	-12.4	-24.2	71.8	-11.3	0	-7.5
1876	CATGATCACAGGCATCAATT SEQ ID NO:593	-12.4	-21.5	63.6	-8.4	-0.4	-6.8
2007	ATCGTTCTTTTTGTGTTCTT SEQ ID NO:594	-12.4	-22.1	68.4	-9.7	0	-3
2925	AAGTAGTAGGATACCCAACA SEQ ID NO:595	-12.4	-21.7	63.6	-8.6	-0.4	-3.7
171	AGGGTCTCCAGGATTTCTCG SEQ ID NO:596	-12.3	-26.5	76.8	-12.9	-1.2	-5.5
215	CAGAATCATATCCTCTGTAC SEQ ID NO:597	-12.3	-21.1	64	-8.1	-0.4	-3.8
312	TCCAGTGCCTTAACTTTTCC SEQ ID NO:598	-12.3	-25.9	73.8	-13.6	0	-3.6
477	ATTCCATTGTGAATAACGAT SEQ ID NO:599	-12.3	-19	57	-6.1	-0.3	-5.2
805	TCCTTTCTTGTCTTTGCCTG SEQ ID NO:600	-12.3	-26.3	77	-14	0	-3
864	GCTTTTTCTTCCACCGGGAA SEQ ID NO:601	-12.3	-26.9	74	-12.8	-1.8	-7.1
970	AAGACGTCCATCCACTACTG SEQ ID NO:602	-12.3	-24.2	68.1	-11.3	0	-8.6
1204	CCGGCATCTCTGGATCTCCT SEQ ID NO:603	-12.3	-29.5	80.9	-16.3	-0.7	-7
1302	AGTTCCACCATCACAGGCAA SEQ ID NO:604	-12.3	-26.3	73.8	-14	0	-4
1538	TATAAGCCTTTGTACTGGCC SEQ ID NO:605	-12.3	-24.6	70.6	-11.1	-1.1	-7.4
2073	GCCAGCAACTGTAAAGGGAT SEQ ID NO:606	-12.3	-23.9	67.5	-10.2	-1.3	-6.8
2074	AGCCAGCAACTGTAAAGGGA SEQ ID NO:607	-12.3	-23.9	67.7	-10.2	-1.3	-6.9
2198	TCTTGTGTTGCTTAATCATA SEQ ID NO:608	-12.3	-20.5	63.6	-8.2	0	-3.6
2208	ACAAAAGGTGTCTTGTGTTG SEQ ID NO:609	-12.3	-20.3	62.1	-6.1	-1.9	-6.1
2926	AAAGTAGTAGGATACCCAAC SEQ ID NO:610	-12.3	-20.3	60.4	-6.9	-1	-4.2
309	AGTGCCTTAACTTTTCCTTT SEQ ID NO:611	-12.2	-23.9	70	-11.7	0	-3
378	GCTATTCCAAGGTGTACATC SEQ ID NO:612	-12.2	-23.5	69.8	-11.3	0	-6.8
430	GGGGTGGCTATTGACAGGAC SEQ ID NO:613	-12.2	-26	75	-13.8	0	-3.7
922	GACGCGATTGGTGTGTTCTA SEQ ID NO:615	-12.2	-24.8	71	-11.7	-0.8	-7.9
1090	TATTTCCTTCTGCATAAATG SEQ ID NO:615	-12.2	-19.4	59.2	-7.2	0	-4.9
1092	AATATTTCCTTCTGCATAAA SEQ ID NO:616	-12.2	-18.7	57.3	-6.5	0	-4.9
1094	CAAATATTTCCTTCTGCATA SEQ ID NO:617	-12.2	-20.1	60.5	-7.9	0	-6
1898	AAGTGTGATCTCTCATGATG SEQ ID NO:618	-12.2	-20.6	63.7	-8.4	0.1	-6.2
2529	TGCACTACTCTTTCACTGGT SEQ ID NO:619	-12.2	-24.5	72.9	-12.3	0	-4.7
2671	TTAAGTTTTACAGTTTGATT SEQ ID NO:620	-12.2	-17.3	56.2	-5.1	0	-2.6
221	CACCAGCAGAATCATATCCT SEQ ID NO:621	-12.1	-24.1	68.5	-12	0	-3.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
421	ATTGACAGGACTGGGTTCTC SEQ ID NO:622	-12.1	-23.9	71.6	-11.8	0	-4.9
818	AGAGATTGCAGCTTCCTTTC SEQ ID NO:623	-12.1	-24.5	73.1	-12.4	0	-5.2
822	CGAGAGAGATTGCAGCTTCC SEQ ID NO:624	-12.1	-25	71.6	-12.9	0	-5.3
1007	GGTGATCTCCTGCAGTTCGT SEQ ID NO:625	-12.1	-27.8	80.3	-15.2	0	-8.2
1198	TCTCTGGATCTCCTTTATGT SEQ ID NO:626	-12.1	-24.1	72.8	-12	0	-5
2349	TCCTCCACAAATTACTGGGA SEQ ID NO:627	-12.1	-23.8	67.2	-11.1	-0.3	-5.9
2856	GCAGCTTGAATTTAAAGTTT SEQ ID NO:628	-12.1	-19.1	58.8	-7	0	-4.9
2921	AGTAGGATACCCAACATGTA SEQ ID NO:629	-12.1	-22.4	65.4	-9.4	-0.8	-8.5
153	CGTCTCGTTCGAGGAACATG SEQ ID NO:630	-12	-23.6	66.5	-9.7	-1.9	-9.1
310	CAGTGCCTTAACTTTTCCTT SEQ ID NO:631	-12	-24.5	70.8	-12.5	0	-3
476	TTCCATTGTGAATAACGATA SEQ ID NO:632	-12	-18.7	56.5	-6.1	-0.3	-3.5
496	GTCTTTGTAGTTGGTGATGA SEQ ID NO:633	-12	-22.5	69.9	-10.5	0	-2.3
1017	GCTCGTCCGGGGTGATCTCC SEQ ID NO:634	-12	-31.4	85.2	-19.4	0	-6.6
1068	CTGAAGTTGCCCTTCATGAT SEQ ID NO:635	-12	-24.6	70.1	-10	-2.6	-8.7
1200	CATCTCTGGATCTCCTTTAT SEQ ID NO:636	-12	-23.6	70.5	-11.1	-0.1	-5.3
1450	TGTGTTTGTGATCCCCACAG SEQ ID NO:637	-12	-26.4	74.9	-12.3	-2.1	-6.5
1645	AGGCAGCCGTTTCAATCCAA SEQ ID NO:638	-12	-26.5	72.5	-13.7	-0.3	-9
1777	TTTCAGTGCCCCTTCAAGAC SEQ ID NO:639	-12	-26.5	74.8	-14.5	0	-3.8
1973	CCTCCTTATCACAAATTACC SEQ ID NO:640	-12	-22.6	64.5	-10.6	0	-3.2
1979	CAGTATCCTCCTTATCACAA SEQ ID NO:641	-12	-23.3	68.1	-11.3	0	-2.7
2851	TTGAATTTAAAGTTTGTGCT SEQ ID NO:642	-12	-17.8	56.2	-5.8	0	-4.8
2924	AGTAGTAGGATACCCAACAT SEQ ID NO:643	-12	-22.4	65.8	-9.5	-0.8	-4.4
187	CTGAAGGCCTTTGATTAGGG SEQ ID NO:644	-11.9	-23.7	68.4	-10.4	-0.3	-10.8
205	TCCTCTGTACTCCAGTCTCT SEQ ID NO:645	-11.9	-27.5	81.9	-14.7	-0.8	-4.8
214	AGAATCATATCCTCTGTACT SEQ ID NO:646	-11.9	-21.3	64.8	-9.4	0	-4.8
249	TCTTTATCATTGCCTCCATC SEQ ID NO:647	-11.9	-24.6	72.2	-12.7	0	-3
1008	GGGTGATCTCCTGCAGTTCG SEQ ID NO:648	-11.9	-27.8	79.3	-15.2	-0.1	-8.7
1190	TCTCCTTTATGTGATCCTTC SEQ ID NO:649	-11.9	-24.1	72.2	-12.2	0	-4.3
1455	CCAACTGTGTTTGTGATCCC SEQ ID NO:650	-11.9	-25.9	73	-14	0	-4.6
2195	TGTGTTGCTTAATCATACAG SEQ ID NO:651	-11.9	-20	61.8	-8.1	0	-1.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2344	CACAAATTACTGGGAAAATG SEQ ID NO:652	-11.9	-16	50.6	-4.1	0	-3.2
2846	TTTAAAGTTTGTGCTATAAA SEQ ID NO:653	-11.9	-15.8	51.7	-3.9	0	-4.3
2858	AAGCAGCTTGAATTTAAAGT SEQ ID NO:654	-11.9	-18.2	56.4	-5.8	0	-7.5
95	AGACACGGCCCGCGAGGCCA SEQ ID NO:655	-11.8	-33.2	81.6	-16.5	-4.7	-17.4
220	ACCAGCAGAATCATATCCTC SEQ ID NO:656	-11.8	-23.8	68.9	-12	0	-4.1
246	TTATCATTGCCTCCATCAAA SEQ ID NO:657	-11.8	-22.5	65	-10.7	0	-3.7
714	CCTCGCCTTGTGCCAACTGC SEQ ID NO:658	-11.8	-30.8	80.8	-18.4	-0.3	-5.2
803	CTTTCTTGTCTTTGCCTGTT SEQ ID NO:659	-11.8	-25.2	75.4	-13.4	0	-3
1971	TCCTTATCACAAATTACCAC SEQ ID NO:660	-11.8	-20.6	60.8	-8.8	0	-3.2
2216	TTTTAAATACAAAAGGTGTC SEQ ID NO:661	-11.8	-15.1	50	-2.6	-0.4	-6.8
2348	CCTCCACAAATTACTGGGAA SEQ ID NO:662	-11.8	-22.7	63.8	-10.3	-0.3	-5.9
2	GTGGCGCCGACACGACTCCC SEQ ID NO:663	-11.7	-32.2	80.7	-18.5	-0.8	-12.1
49	GTGCACACACGAGCTTCGGT SEQ ID NO:664	-11.7	-27.5	75.9	-13.8	-1.6	-11.7
209	CATATCCTCTGTACTCCAGT SEQ ID NO:665	-11.7	-25.3	74.3	-12.7	-0.8	-4.8
336	TCTTGTTGCTTGTGAACTTC SEQ ID NO:666	-11.7	-22.2	67.9	-10	-0.1	-4.9
492	TTGTAGTTGGTGATGATTCC SEQ ID NO:667	-11.7	-22.4	68.2	-10.7	0	-2.6
1456	GCCAACTGTGTTTGTGATCC SEQ ID NO:668	-11.7	-25.7	73.7	-14	0	-4.9
1638	CGTTTCAATCCAAGCATGAT SEQ ID NO:669	-11.7	-22.1	63.5	-10.4	0	-4.8
1646	CAGGCAGCCGTTTCAATCCA SEQ ID NO:670	-11.7	-27.9	75.9	-15.4	-0.3	-9
1807	TTCAGAGTGCATATAAGTAA SEQ ID NO:671	-11.7	-18.4	58.1	-6.7	0	-5.4
2459	TCTCAGATTGAAGTGGAGGG SEQ ID NO:672	-11.7	-22.4	67.5	-10.7	0	-4.3
977	GGATAGAAAGACGTCCATCC SEQ ID NO:673	-11.6	-23	65.4	-10.7	-0.3	-8.6
1016	CTCGTCCGGGGTGATCTCCT SEQ ID NO:674	-11.6	-30.5	82.7	-18	-0.8	-6
1639	CCGTTTCAATCCAAGCATGA SEQ ID NO:675	-11.6	-24.1	67	-12.5	0	-4.8
1721	CTGACTTCTGATGATAAAGT SEQ ID NO:676	-11.6	-18.7	58.1	-6.4	-0.5	-4
1806	TCAGAGTGCATATAAGTAAT SEQ ID NO:677	-11.6	-18.3	57.8	-6.7	0	-5.9
1808	CTTCAGAGTGCATATAAGTA SEQ ID NO:678	-11.6	-20	62.3	-8.4	0	-5.4
2554	ACTGGCTTTAGATACTCCAA SEQ ID NO:679	-11.6	-22.7	66.7	-11.1	0	-3.7
2570	ATGAGCATACACTGCCACTG SEQ ID NO:680	-11.6	-24.4	69.5	-11.1	-1.7	-5
2572	GTATGAGCATACACTGCCAC SEQ ID NO:681	-11.6	-24.4	70.4	-11.1	-1.7	-8.9

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2674	GTTTTAAGTTTTACAGTTTG SEQ ID NO:682	-11.6	-18	58.4	-6.4	0	-2.6
2675	AGTTTTAAGTTTTACAGTTT SEQ ID NO:683	-11.6	-18	58.7	-6.4	0	-2.6
2850	TGAATTTAAAGTTTGTGCTA SEQ ID NO:684	-11.6	-17.4	55.3	-5.8	0	-4.9
1	TGGCGCCGACACGACTCCCT SEQ ID NO:685	-11.5	-31.9	79.3	-18.5	-0.1	-12
191	GTCTCTGAAGGCCTTTGATT SEQ ID NO:686	-11.5	-24.5	72	-11.6	0	-10.8
455	ATTCATTATTTTTATCAGAG SEQ ID NO:687	-11.5	-16.8	55.2	-5.3	0	-2.8
874	ATACTCCACTGCTTTTTCTT SEQ ID NO:688	-11.5	-23.5	70	-12	0	-3.6
1872	ATCACAGGCATCAATTTATC SEQ ID NO:689	-11.5	-20.4	62.3	-8.9	0	-4
2567	AGCATACACTGCCACTGGCT SEQ ID NO:690	-11.5	-27.7	77.1	-14.1	-2.1	-9.7
2842	AAGTTTGTGCTATAAAATTG SEQ ID NO:691	-11.5	-16	51.9	-4.5	0	-3.8
152	GTCTCGTTCGAGGAACATGG SEQ ID NO:692	-11.4	-24	68.9	-11.1	-1.4	-9.1
241	ATTGCCTCCATCAAATCCCA SEQ ID NO:693	-11.4	-26.7	72.1	-15.3	0	-3.7
393	GCCCAACGGGTATGAGCTAT SEQ ID NO:694	-11.4	-27.1	73.4	-14.4	-1.2	-8
400	ATGTGTTGCCCAACGGGTAT SEQ ID NO:695	-11.4	-26.6	73	-13.9	-1.2	-7.7
425	GGCTATTGACAGGACTGGGT SEQ ID NO:696	-11.4	-25.7	74.4	-14.3	0	-5.8
559	AATTGTCTCTGTGTCTGTTT SEQ ID NO:697	-11.4	-22.3	69.7	-10.9	0	-2.3
808	GCTTCCTTTCTTGTCTTTGC SEQ ID NO:698	-11.4	-26.2	78.5	-14.8	0	-2.8
1452	ACTGTGTTTGTGATCCCCAC SEQ ID NO:699	-11.4	-26.8	76	-14.5	-0.8	-4.3
1643	GCAGCCGTTTCAATCCAAGC SEQ ID NO:700	-11.4	-27.1	74.2	-15.7	0	-3.5
1880	TGATCATGATCACAGGCATC SEQ ID NO:701	-11.4	-22.4	66.9	-8.4	-0.6	-13.4
1996	TGTGTTCTTAATGGTCTCAG SEQ ID NO:702	-11.4	-21.7	67.4	-10.3	0	-2.4
2070	AGCAACTGTAAAGGGATCAC SEQ ID NO:703	-11.4	-20.7	61.8	-8.6	-0.4	-6.4
2404	ATAATAGCTAGAATCTTTCT SEQ ID NO:704	-11.4	-17.8	56.9	-5.7	-0.5	-6.8
2471	AACATATTGTCTTCTCAGAT SEQ ID NO:705	-11.4	-19.6	61.4	-7.7	-0.2	-3.1
2487	AGTACCAATTTTTAGAAACA SEQ ID NO:706	-11.4	-17.3	54.3	-5.9	0	-4.4
2553	CTGGCTTTAGATACTCCAAT SEQ ID NO:707	-11.4	-22.5	66.1	-11.1	0	-3.7
2571	TATGAGCATACACTGCCACT SEQ ID NO:708	-11.4	-24.1	69.1	-11.1	-1.6	-6.3
2843	AAAGTTTGTGCTATAAAATT SEQ ID NO:709	-11.4	-15.3	50.3	-3.9	0	-4.1
308	GTGCCTTAACTTTTCCTTTC SEQ ID NO:710	-11.3	-24.3	71.4	-13	0	-3
440	CAGAGCGCTGGGGGTGGCTA SEQ ID NO:711	-11.3	-30.2	82.9	-17.9	-0.8	-9.4

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
610	GCTGGTATCTTGACTTTCCC SEQ ID NO:712	-11.3	-26.5	76.6	-15.2	0	-2.8
1449	GTGTTTGTGATCCCCACAGT SEQ ID NO:713	-11.3	-27.6	78.6	-14.5	-1.8	-7.1
1493	TATGAACTCCACAATCTGTC SEQ ID NO:715	-11.3	-20.9	62.7	-9.6	0	-2.6
1577	TCATAAGGGCAAACATCACA SEQ ID NO:715	-11.3	-20.5	60.5	-9.2	0	-4
1722	ACTGACTTCTGATGATAAAG SEQ ID NO:716	-11.3	-17.7	55.7	-6.4	0	-2.9
1805	CAGAGTGCATATAAGTAATT SEQ ID NO:717	-11.3	-18	56.7	-6.7	0	-5.5
1908	CACTTGGCATAAGTGTGATC SEQ ID NO:718	-11.3	-22	66	-8.2	-2.5	-7.9
2228	TTTAAATCAAGGTTTTAAAT SEQ ID NO:719	-11.3	-13.9	47.5	-1.4	-1	-4.6
2229	TTTTAAATCAAGGTTTTAAA SEQ ID NO:720	-11.3	-14	47.7	-1.4	-1.1	-4.8
2517	TCACTGGTCTGAATGAAGTA SEQ ID NO:721	-11.3	-20.6	62.8	-9.3	0	-3
2762	TTTCTTCCACCTACAGATAA SEQ ID NO:722	-11.3	-22	64.9	-10.7	0	-2.4
2930	ACACAAAGTAGTAGGATACC SEQ ID NO:723	-11.3	-19.9	60.5	-7.7	-0.8	-4.3
2939	GAGATGAAAACACAAAGTAG SEQ ID NO:724	-11.3	-15	49.2	-3.7	0	-2.9
190	TCTCTGAAGGCCTTTGATTA SEQ ID NO:725	-11.2	-23	68	-10.4	0	-10.8
216	GCAGAATCATATCCTCTGTA SEQ ID NO:726	-11.2	-22.7	67.7	-10.3	-1.1	-4.9
401	CATGTGTTGCCCAACGGGTA SEQ ID NO:727	-11.2	-27.3	74	-14.8	-1.2	-7
475	TCCATTGTGAATAACGATAA SEQ ID NO:728	-11.2	-17.9	54.5	-6.1	-0.3	-3.5
601	TTGACTTTCCCGATTGTCAT SEQ ID NO:729	-11.2	-24.2	69.1	-11.7	-1.2	-5.6
935	CTTCCAGAAAGATGACGCGA SEQ ID NO:730	-11.2	-22.7	63.3	-11	0	-7.9
976	GATAGAAAGACGTCCATCCA SEQ ID NO:731	-11.2	-22.5	64.2	-10.7	0	-8.6
1873	GATCACAGGCATCAATTTAT SEQ ID NO:732	-11.2	-20.6	62.2	-9.4	0	-4.7
1882	GATGATCATGATCACAGGCA SEQ ID NO:733	-11.2	-22.6	66.7	-8.4	-1	-14.2
1899	TAAGTGTGATCTCTCATGAT SEQ ID NO:734	-11.2	-20.3	63.2	-8.4	-0.4	-6.2
1900	ATAAGTGTGATCTCTCATGA SEQ ID NO:735	-11.2	-20.3	63.2	-8.4	-0.4	-5.9
1904	TGGCATAAGTGTGATCTCTC SEQ ID NO:736	-11.2	-22.7	69.1	-11.5	0	-6.5
2458	CTCAGATTGAAGTGGAGGGT SEQ ID NO:737	-11.2	-23.2	69.2	-12	0	-3.9
2672	TTTAAGTTTTACAGTTTGAT SEQ ID NO:738	-11.2	-17.3	56.2	-6.1	0	-2.6
2761	TTCTTCCACCTACAGATAAT SEQ ID NO:739	-11.2	-21.9	64.5	-10.7	0	-2.4
2929	CACAAAGTAGTAGGATACCC SEQ ID NO:740	-11.2	-21.7	63.6	-9.6	-0.8	-4.3
3055	ATTAATTTAATAGCAGCTCT SEQ ID NO:741	-11.2	-18.5	58	-7.3	0	-6.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
188	TCTGAAGGCCTTTGATTAGG SEQ ID NO:742	-11.1	-22.9	67.4	-10.4	0	-10.8
189	CTCTGAAGGCCTTTGATTAG SEQ ID NO:743	-11.1	-22.6	66.7	-10.4	0	-10.2
609	CTGGTATCTTGACTTTCCCG SEQ ID NO:744	-11.1	-25.5	72.1	-14.4	0	-3.2
1336	GACTGGTGTGTTTCTGTCCA SEQ ID NO:745	-11.1	-26.3	78.2	-15.2	0	-3.6
1596	GAGATCCGATCATCACACAT SEQ ID NO:746	-11.1	-23	66.2	-11	-0.7	-7.5
1895	TGTGATCTCTCATGATGATC SEQ ID NO:747	-11.1	-21.1	65.4	-8.4	-1.4	-10.3
2067	AACTGTAAAGGGATCACGCT SEQ ID NO:748	-11.1	-21.7	62.7	-9.2	-1.3	-6.6
2678	TTCAGTTTTAAGTTTTACAG SEQ ID NO:749	-11.1	-17.8	57.9	-6.7	0	-2.6
2845	TTAAAGTTTGTGCTATAAAA SEQ ID NO:750	-11.1	-15	49.7	-3.9	0	-4.3
78	CCAGGGGCGAGTGGCTGGCG SEQ ID NO:751	-11	-32.4	84.3	-19.7	-1.7	-8
137	CATGGTAGTTTAAGTAAGCA SEQ ID NO:752	-11	-19.9	61.5	-8.9	0	-4.1
238	GCCTCCATCAAATCCCACAC SEQ ID NO:753	-11	-27.7	74	-16.7	0	-2
242	CATTGCCTCCATCAAATCCC SEQ ID NO:754	-11	-26.7	72.1	-15.7	0	-3.7
382	ATGAGCTATTCCAAGGTGTA SEQ ID NO:755	-11	-22.8	67.9	-11.8	0	-5.1
383	TATGAGCTATTCCAAGGTGT SEQ ID NO:756	-11	-22.8	67.9	-11.8	0	-5.1
481	GATGATTCCATTGTGAATAA SEQ ID NO:757	-11	-18.6	57	-6.9	-0.5	-6.1
1006	GTGATCTCCTGCAGTTCGTT SEQ ID NO:758	-11	-26.7	78	-15.2	0	-8.2
1205	GCCGGCATCTCTGGATCTCC SEQ ID NO:759	-11	-30.4	83.3	-17.6	-0.9	-11.6
1299	TCCACCATCACAGGCAACTC SEQ ID NO:760	-11	-26.5	73.9	-14.6	-0.8	-4.5
1698	GTTGCTAGTTTCTGAATTTC SEQ ID NO:761	-11	-20.9	65.5	-9.9	0	-4.7
1871	TCACAGGCATCAATTTATCC SEQ ID NO:762	-11	-22.4	66.2	-11.4	0	-4
2075	AAGCCAGCAACTGTAAAGGG SEQ ID NO:763	-11	-22.6	64.4	-10.2	-1.3	-6.9
2530	ATGCACTACTCTTTCACTGG SEQ ID NO:764	-11	-23.3	69.4	-12.3	0	-5.5
2844	TAAAGTTTGTGCTATAAAAT SEQ ID NO:765	-11	-14.9	49.4	-3.9	0	-4.3
2879	AATCATATTGTCAGTTGTCC SEQ ID NO:766	-11	-21.4	65.8	-10.4	0	-2.1
77	CAGGGGCGAGTGGCTGGCGG SEQ ID NO:767	-10.9	-31.6	83.5	-19.7	-0.9	-6.3
120	GCAAATATACCACACATGAT SEQ ID NO:768	-10.9	-19.8	58.4	-8.9	0	-5.2
121	AGCAAATATACCACACATGA SEQ ID NO:769	-10.9	-19.8	58.6	-8.9	0	-5.2
185	GAAGGCCTTTGATTAGGGTC SEQ ID NO:770	-10.9	-24.4	71.5	-11.5	0.3	-12.1
381	TGAGCTATTCCAAGGTGTAC SEQ ID NO:771	-10.9	-23	68.5	-12.1	0	-5.1

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
416	CAGGACTGGGTTCTCCATGT SEQ ID NO:772	-10.9	-26.9	77.7	-14.7	-1.2	-5.8
817	GAGATTGCAGCTTCCTTTCT SEQ ID NO:773	-10.9	-25.4	74.8	-14.5	0	-4.9
1070	AACTGAAGTTGCCCTTCATG SEQ ID NO:774	-10.9	-23.5	67.2	-10	-2.6	-8.7
1156	CACAGTATAGTCATCAAAGT SEQ ID NO:775	-10.9	-19.4	60.6	-8.5	0	-2.7
1300	TTCCACCATCACAGGCAACT SEQ ID NO:776	-10.9	-26.2	72.6	-14.4	-0.7	-4.4
1494	ATATGAACTCCACAATCTGT SEQ ID NO:777	-10.9	-20.5	61.3	-9.6	0	-2.5
2183	TCATACAGTTTCGTACATTT SEQ ID NO:778	-10.9	-20.3	62.4	-8.9	-0.1	-4.8
2511	GTCTGAATGAAGTATGGTGA SEQ ID NO:779	-10.9	-20.2	62	-9.3	0	-3
2526	ACTACTCTTTCACTGGTCTG SEQ ID NO:780	-10.9	-23.3	70.9	-12.4	0	-2.5
2528	GCACTACTCTTTCACTGGTC SEQ ID NO:781	-10.9	-24.9	74.9	-14	0	-3.4
456	AATTCATTATTTTTATCAGA SEQ ID NO:782	-10.8	-16.1	53.1	-5.3	0	-2.7
566	GCTTGGCAATTGTCTCTGTG SEQ ID NO:783	-10.8	-24.9	73.6	-13.6	0	-8.3
625	CACCAAGGTAGTAAAGCTGG SEQ ID NO:784	-10.8	-22.4	65	-11.6	0	-5.1
633	ACTCTCTCCACCAAGGTAGT SEQ ID NO:785	-10.8	-26.3	76.2	-15	-0.2	-5.1
851	CCGGGAAAAGGCAGGTTGTG SEQ ID NO:786	-10.8	-25.1	68.8	-14.3	0	-5.6
918	CGATTGGTGTGTTCTATGAC SEQ ID NO:787	-10.8	-22.2	66.5	-11.4	0	-2.1
969	AGACGTCCATCCACTACTGC SEQ ID NO:788	-10.8	-26.7	74.5	-15.3	0	-8.6
974	TAGAAAGACGTCCATCCACT SEQ ID NO:789	-10.8	-23	65.3	-11.6	0	-8.6
975	ATAGAAAGACGTCCATCCAC SEQ ID NO:790	-10.8	-22.1	63.4	-10.7	0	-8.6
1093	AAATATTTCCTTCTGCATAA SEQ ID NO:791	-10.8	-18.7	57.3	-7.9	0	-5.8
1597	GGAGATCCGATCATCACACA SEQ ID NO:792	-10.8	-24.2	68.7	-12.5	-0.7	-7.5
2184	ATCATACAGTTTCGTACATT SEQ ID NO:793	-10.8	-20.2	62.1	-8.9	-0.1	-4.8
2345	CCACAAATTACTGGGAAAAT SEQ ID NO:794	-10.8	-18	54	-7.2	0	-4.9
2852	CTTGAATTTAAAGTTTGTGC SEQ ID NO:795	-10.8	-17.8	56.2	-7	0	-4.9
130	GTTTAAGTAAGCAAATATAC SEQ ID NO:796	-10.7	-15.3	50.6	-4.6	0	-4.1
411	CTGGGTTCTCCATGTGTTGC SEQ ID NO:797	-10.7	-27.3	79.8	-15.3	-1.2	-4.7
412	ACTGGGTTCTCCATGTGTTG SEQ ID NO:798	-10.7	-25.7	75.8	-13.7	-1.2	-4.5
474	CCATTGTGAATAACGATAAA SEQ ID NO:799	-10.7	-16.8	51.8	-6.1	0	-3.5
499	CAAGTCTTTGTAGTTGGTGA SEQ ID NO:800	-10.7	-21.9	67.6	-11.2	0	-2.6
553	CTCTGTGTCTGTTTCAGATT SEQ ID NO:801	-10.7	-23.1	71.8	-10.9	-1.4	-6.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
619	GGTAGTAAAGCTGGTATCTT SEQ ID NO:802	-10.7	-21.8	66.7	-11.1	0	-5.1
875	AATACTCCACTGCTTTTTCT SEQ ID NO:803	-10.7	-22.7	67.3	-12	0	-3.6
1012	TCCGGGGTGATCTCCTGCAG SEQ ID NO:804	-10.7	-29.7	81.5	-18.1	-0.8	-8.4
1152	GTATAGTCATCAAAGTTGAC SEQ ID NO:805	-10.7	-18.7	59.4	-7.3	-0.4	-6
1521	GCCACACCAATCTCAGGACC SEQ ID NO:806	-10.7	-28	75.9	-17.3	0	-3.7
1800	TGCATATAAGTAATTTCTTT SEQ ID NO:807	-10.7	-17.1	55	-5.9	-0.2	-4.9
1816	AAGGATGCCTTCAGAGTGCA SEQ ID NO:808	-10.7	-25.3	72.8	-13.4	-1.1	-7
1867	AGGCATCAATTTATCCACCA SEQ ID NO:809	-10.7	-24	68.3	-13.3	0	-4
2010	TTGATCGTTCTTTTTGTGTT SEQ ID NO:810	-10.7	-21.4	66	-10.7	0	-5.3
2470	ACATATTGTCTTCTCAGATT SEQ ID NO:811	-10.7	-20.4	64	-9.2	-0.2	-2.8
2527	CACTACTCTTTCACTGGTCT SEQ ID NO:812	-10.7	-24	72.3	-13.3	0	-2.5
2664	TTACAGTTTGATTTAAAAAC SEQ ID NO:813	-10.7	-14	47.7	-3.3	0.2	-5.2
3063	ATATCAATATTAATTTAATA SEQ ID NO:815	-10.7	-11.8	43.4	-0.2	-0.2	-6.8
96	GAGACACGGCCCGCGAGGCC SEQ ID NO:815	-10.6	-33.1	81.9	-18.4	-3.6	-16
527	CATAGCCTTTGCTTTCCAAA SEQ ID NO:816	-10.6	-23.9	67.8	-11.9	-1.3	-4.8
620	AGGTAGTAAAGCTGGTATCT SEQ ID NO:817	-10.6	-21.7	66.6	-11.1	0	-5.1
637	GATAACTCTCTCCACCAAGG SEQ ID NO:818	-10.6	-23.8	68.1	-13.2	0	-3.6
1003	ATCTCCTGCAGTTCGTTTAA SEQ ID NO:819	-10.6	-24	70.4	-12.9	0	-7.7
1578	ATCATAAGGGCAAACATCAC SEQ ID NO:820	-10.6	-19.8	59.3	-9.2	0	-4
1866	GGCATCAATTTATCCACCAA SEQ ID NO:821	-10.6	-23.3	65.9	-12.7	0	-4
1881	ATGATCATGATCACAGGCAT SEQ ID NO:822	-10.6	-22	65.4	-8.4	-1	-14.2
2469	CATATTGTCTTCTCAGATTG SEQ ID NO:823	-10.6	-20.2	63.3	-9.1	-0.2	-3.6
2552	TGGCTTTAGATACTCCAATT SEQ ID NO:824	-10.6	-21.7	64.5	-11.1	0	-3.7
2586	CCCTAACTGTCCAAGTATGA SEQ ID NO:825	-10.6	-24.1	68.1	-13.5	0	-3
2673	TTTTAAGTTTTACAGTTTGA SEQ ID NO:826	-10.6	-17.4	56.6	-6.8	0	-2.6
3062	TATCAATATTAATTTAATAG SEQ ID NO:827	-10.6	-11.8	43.4	-0.2	-0.4	-7.1
24	ATCTGCGGGCTCGGGGGCCG SEQ ID NO:828	-10.5	-33.6	85.3	-19.5	-3.6	-11.8
36	CTTCGGTGGGCAATCTGCGG SEQ ID NO:829	-10.5	-27.9	75.6	-15.2	-2.2	-6.6
94	GACACGGCCCGCGAGGCCAG SEQ ID NO:830	-10.5	-33.2	81.6	-18.1	-4.2	-16.9
108	CACATGATGCCGGAGACACG SEQ ID NO:831	-10.5	-25.1	67.7	-14.6	0	-6.7

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
138	ACATGGTAGTTTAAGTAAGC SEQ ID NO:832	-10.5	-19.4	60.8	-8.9	0	-5.2
174	ATTAGGGTCTCCAGGATTTC SEQ ID NO:833	-10.5	-24.2	72.9	-12.5	-1.1	-5.4
433	CTGGGGGTGGCTATTGACAG SEQ ID NO:834	-10.5	-26.1	74.9	-15.6	0	-3.7
936	TCTTCCAGAAAGATGACGCG SEQ ID NO:835	-10.5	-22.5	63.4	-11	-0.8	-9
1325	TTCTGTCCAGGAAGTCACTT SEQ ID NO:836	-10.5	-24.3	72.4	-13.3	0	-7.5
1453	AACTGTGTTTGTGATCCCCA SEQ ID NO:837	-10.5	-25.9	73	-15.4	0	-4.3
1776	TTCAGTGCCCCTTCAAGACA SEQ ID NO:838	-10.5	-27.1	75.5	-16.6	0	-3.8
1809	CCTTCAGAGTGCATATAAGT SEQ ID NO:839	-10.5	-22.3	66.8	-11.8	0	-5.4
1883	TGATGATCATGATCACAGGC SEQ ID NO:840	-10.5	-21.9	65.4	-8.4	-1	-14.2
1997	TTGTGTTCTTAATGGTCTCA SEQ ID NO:841	-10.5	-21.8	67.6	-11.3	0	-2.4
2006	TCGTTCTTTTTGTGTTCTTA SEQ ID NO:842	-10.5	-21.8	67.8	-11.3	0	-3
2227	TTAAATCAAGGTTTTAAATA SEQ ID NO:843	-10.5	-13.5	46.7	-3	0	-4.5
2302	CACATATTGAGTGGAATAAT SEQ ID NO:844	-10.5	-17.3	54.4	-6.3	-0.1	-4.2
2311	CACAAAAATCACATATTGAG SEQ ID NO:845	-10.5	-15.2	49.4	-4.1	-0.3	-4.5
2538	CCAATTAAATGCACTACTCT SEQ ID NO:846	-10.5	-20.1	59.5	-9.6	0	-5.5
2573	AGTATGAGCATACACTGCCA SEQ ID NO:847	-10.5	-24.2	70.1	-12	-1.7	-9.6
2968	AGATACAAGGAAATAAAAAA SEQ ID NO:848	-10.5	-11.1	41.4	-0.3	0	-1.3
250	ATCTTTATCATTGCCTCCAT SEQ ID NO:849	-10.4	-24.2	70.5	-13.8	0	-3
337	ATCTTGTTGCTTGTGAACTT SEQ ID NO:850	-10.4	-21.8	66.3	-11.4	0.6	-4.2
567	AGCTTGGCAATTGTCTCTGT SEQ ID NO:851	-10.4	-24.9	74.1	-13.6	-0.7	-7.6
923	TGACGCGATTGGTGTGTTCT SEQ ID NO:852	-10.4	-25.1	71.5	-13.8	-0.8	-7.9
1126	TCTCATTGTGTTCACGACAG SEQ ID NO:853	-10.4	-22.6	67.6	-11.3	-0.7	-6.4
1201	GCATCTCTGGATCTCCTTTA SEQ ID NO:854	-10.4	-25.4	75.1	-14.5	-0.1	-5.3
1203	CGGCATCTCTGGATCTCCTT SEQ ID NO:855	-10.4	-27.6	77.7	-16.3	-0.7	-5.3
1232	TTGTTCCACAAGCAATAAGA SEQ ID NO:856	-10.4	-20.1	60	-8.8	-0.7	-5.8
1765	TTCAAGACAAGTAGCATAAT SEQ ID NO:857	-10.4	-17.7	55.6	-7.3	0	-4.1
1874	TGATCACAGGCATCAATTTA SEQ ID NO:858	-10.4	-20.6	62.1	-10.2	0	-6
2301	ACATATTGAGTGGAATAATT SEQ ID NO:859	-10.4	-16.7	53.4	-6.3	0	-3
2315	ACTTCACAAAAATCACATAT SEQ ID NO:860	-10.4	-16.1	51.4	-5.7	0	-1.8
2350	GTCCTCCACAAATTACTGGG SEQ ID NO:861	-10.4	-24.4	69.1	-14	0.3	-5.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2964	ACAAGGAAATAAAAAACACT SEQ ID NO:862	-10.4	-12.8	44.4	-2.4	0	-2.1
82	GAGGCCAGGGGCGAGTGGCT SEQ ID NO:863	-10.3	-32.2	86.9	-18.6	-3.3	-9.8
213	GAATCATATCCTCTGTACTC SEQ ID NO:864	-10.3	-21.7	66.1	-11.4	0	-4.8
560	CAATTGTCTCTGTGTCTGTT SEQ ID NO:865	-10.3	-22.9	70.5	-12.6	0	-5.5
600	TGACTTTCCCGATTGTCATA SEQ ID NO:866	-10.3	-23.8	68.1	-12.4	-1	-5.2
713	CTCGCCTTGTGCCAACTGCT SEQ ID NO:867	-10.3	-29.7	79.4	-18.4	-0.9	-6.1
715	ACCTCGCCTTGTGCCAACTG SEQ ID NO:868	-10.3	-29.2	77.3	-18.4	-0.1	-4.6
871	CTCCACTGCTTTTTCTTCCA SEQ ID NO:869	-10.3	-26.7	76.6	-16.4	0	-3.6
877	GTAATACTCCACTGCTTTTT SEQ ID NO:870	-10.3	-22.3	66.4	-12	0	-3.6
933	TCCAGAAAGATGACGCGATT SEQ ID NO:871	-10.3	-21.8	61.5	-11	0	-7.9
934	TTCCAGAAAGATGACGCGAT SEQ ID NO:872	-10.3	-21.8	61.5	-11	0	-7.9
968	GACGTCCATCCACTACTGCT SEQ ID NO:873	-10.3	-27.6	76.1	-17.3	0	-7.4
1002	TCTCCTGCAGTTCGTTTAAT SEQ ID NO:874	-10.3	-24	70.4	-13.2	0	-8.2
1004	GATCTCCTGCAGTTCGTTTA SEQ ID NO:875	-10.3	-25.3	74.3	-14.5	0	-8.2
1155	ACAGTATAGTCATCAAAGTT SEQ ID NO:876	-10.3	-18.8	59.6	-8.5	0	-2.5
1580	ACATCATAAGGGCAAACATC SEQ ID NO:877	-10.3	-19.8	59.3	-9.5	0	-4
1644	GGCAGCCGTTTCAATCCAAG SEQ ID NO:878	-10.3	-26.5	72.5	-15.7	0	-8.3
1647	TCAGGCAGCCGTTTCAATCC SEQ ID NO:879	-10.3	-27.6	76.5	-16.5	-0.3	-9
1767	CCTTCAAGACAAGTAGCATA SEQ ID NO:880	-10.3	-21.3	63.3	-11	0	-4.1
1891	ATCTCTCATGATGATCATGA SEQ ID NO:881	-10.3	-20.6	63.4	-7.2	-3.1	-10.6
2551	GGCTTTAGATACTCCAATTA SEQ ID NO:882	-10.3	-21.4	64	-11.1	0	-3.7
2920	GTAGGATACCCAACATGTAC SEQ ID NO:883	-10.3	-22.6	65.7	-11.2	-1	-8.1
2963	CAAGGAAATAAAAAACACTT SEQ ID NO:884	-10.3	-12.7	44.2	-2.4	0	-2.8
426	TGGCTATTGACAGGACTGGG SEQ ID NO:885	-10.2	-24.5	70.8	-14.3	0	-5.8
427	GTGGCTATTGACAGGACTGG SEQ ID NO:886	-10.2	-24.5	71.5	-14.3	0	-5.8
878	AGTAATACTCCACTGCTTTT SEQ ID NO:887	-10.2	-22.2	66.3	-12	0	-4.9
1158	TTCACAGTATAGTCATCAAA SEQ ID NO:888	-10.2	-18.7	59	-8.5	0	-2.7
1168	ACCACCCAAATTCACAGTAT SEQ ID NO:889	-10.2	-23.4	65.7	-13.2	0	-3.1
1189	CTCCTTTATGTGATCCTTCA SEQ ID NO:890	-10.2	-24.4	71.7	-13.6	-0.3	-5.5
1333	TGGTGTGTTTCTGTCCAGGA SEQ ID NO:891	-10.2	-26.4	78.6	-16.2	0	-5.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1576	CATAAGGGCAAACATCACAA SEQ ID NO:892	-10.2	-19.4	57.4	-9.2	0	-4
1804	AGAGTGCATATAAGTAATTT SEQ ID NO:893	-10.2	-17.4	55.8	-6.7	-0.2	-6.1
2131	TTTGGCAAGATTCCGTGGGA SEQ ID NO:894	-10.2	-25.3	70.8	-14.6	-0.1	-4.4
2363	TCCATTATTCAAAGTCCTCC SEQ ID NO:895	-10.2	-23.6	68.4	-13.4	0	-1.6
2518	TTCACTGGTCTGAATGAAGT SEQ ID NO:896	-10.2	-21	63.8	-10.3	-0.2	-4.3
2559	CTGCCACTGGCTTTAGATAC SEQ ID NO:897	-10.2	-24.8	71.5	-12.5	-2.1	-9.7
2694	CCTACCAATAAAATTTTTCA SEQ ID NO:898	-10.2	-17.9	54.5	-7.7	0	-6.7
4	GGGTGGCGCCGACACGACTC SEQ ID NO:899	-10.1	-30.6	79.1	-18.4	-1.6	-12.1
26	CAATCTGCGGGCTCGGGGGC SEQ ID NO:900	-10.1	-30.8	81.1	-19.8	-0.7	-8.1
103	GATGCCGGAGACACGGCCCG SEQ ID NO:901	-10.1	-31.3	77.6	-17.1	-4.1	-10.6
126	AAGTAAGCAAATATACCACA SEQ ID NO:902	-10.1	-17.8	54.6	-7.7	0	-4.1
304	CTTAACTTTTCCTTTCTTCT SEQ ID NO:903	-10.1	-21.6	66	-11.5	0	-2.2
422	TATTGACAGGACTGGGTTCT SEQ ID NO:904	-10.1	-23.2	69.3	-13.1	0	-5.8
462	ACGATAAATTCATTATTTTT SEQ ID NO:905	-10.1	-15.3	50.2	-4.5	-0.5	-3.8
647	CCAATTGTTGGATAACTCTC SEQ ID NO:906	-10.1	-21	62.7	-9.5	-1.3	-6.3
655	AGCACCTTCCAATTGTTGGA SEQ ID NO:907	-10.1	-25.3	71.6	-12.7	-2.5	-9.1
705	GTGCCAACTGCTTGCCCGGG SEQ ID NO:908	-10.1	-31.9	82.1	-20.1	-0.9	-11.5
717	CTACCTCGCCTTGTGCCAAC SEQ ID NO:909	-10.1	-28.9	77	-18.2	-0.3	-4.6
725	ACAGAGGGCTACCTCGCCTT SEQ ID NO:910	-10.1	-29.4	79.9	-15.4	-3.9	-9.6
802	TTTCTTGTCTTTGCCTGTTC SEQ ID NO:911	-10.1	-24.7	75.2	-14.6	0	-3
882	GCAAAGTAATACTCCACTGC SEQ ID NO:912	-10.1	-22.1	64.4	-12	0	-5.6
885	GAAGCAAAGTAATACTCCAC SEQ ID NO:913	-10.1	-19.3	58.1	-9.2	0	-5.6
1056	TTCATGATCTGCTGGAGTTC SEQ ID NO:915	-10.1	-23.3	70.9	-13.2	0	-7.1
1157	TCACAGTATAGTCATCAAAG SEQ ID NO:915	-10.1	-18.6	58.8	-8.5	0	-2.5
1202	GGCATCTCTGGATCTCCTTT SEQ ID NO:916	-10.1	-26.9	78.5	-16.3	-0.2	-5.3
1213	AATCAAACGCCGGCATCTCT SEQ ID NO:917	-10.1	-24.9	67.4	-13.1	0	-11.6
1454	CAACTGTGTTTGTGATCCCC SEQ ID NO:918	-10.1	-25.9	73	-15.8	0	-4.3
1598	TGGAGATCCGATCATCACAC SEQ ID NO:919	-10.1	-23.5	67.5	-12.5	-0.7	-7.5
1602	TGCATGGAGATCCGATCATC SEQ ID NO:920	-10.1	-24.2	69.2	-13.2	-0.7	-7.5
1831	TTTCAATTCACCAGCAAGGA SEQ ID NO:921	-10.1	-22.3	65	-11.4	-0.6	-4.9

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2457	TCAGATTGAAGTGGAGGGTC SEQ ID NO:922	-10.1	-22.7	68.8	-12.6	0	-2.5
2928	ACAAAGTAGTAGGATACCCA SEQ ID NO:923	-10.1	-21.7	63.6	-10.5	-1	-4.1
54	CGGGGGTGCACACACGAGCT SEQ ID NO:924	-10	-29.4	78	-17.8	-1.6	-9
76	AGGGGCGAGTGGCTGGCGGG SEQ ID NO:925	-10	-32.1	85	-20.4	-1.7	-6.3
480	ATGATTCCATTGTGAATAAC SEQ ID NO:926	-10	-18.2	56.3	-7.5	-0.5	-6.1
498	AAGTCTTTGTAGTTGGTGAT SEQ ID NO:927	-10	-21.2	66.3	-11.2	0	-2.4
605	TATCTTGACTTTCCCGATTG SEQ ID NO:928	-10	-22.9	66.1	-12.9	0	-2.8
1015	TCGTCCGGGGTGATCTCCTG SEQ ID NO:929	-10	-29.6	80.6	-18.7	-0.8	-6.6
1077	ATAAATGAACTGAAGTTGCC SEQ ID NO:930	-10	-18.3	55.8	-8.3	0	-5.7
1159	ATTCACAGTATAGTCATCAA SEQ ID NO:931	-10	-19.4	61.1	-9.4	0	-2.7
1498	ATTAATATGAACTCCACAAT SEQ ID NO:932	-10	-17.1	53.3	-7.1	0	-5
1697	TTGCTAGTTTCTGAATTTCG SEQ ID NO:933	-10	-20.5	62.5	-10.5	0	-5
1815	AGGATGCCTTCAGAGTGCAT SEQ ID NO:934	-10	-26	75.3	-13.4	-2.6	-6.8
2008	GATCGTTCTTTTTGTGTTCT SEQ ID NO:935	-10	-22.6	69.5	-12.6	0	-4.7
2012	CCTTGATCGTTCTTTTTGTG SEQ ID NO:936	-10	-23	68.1	-13	0	-5.3
2185	AATCATACAGTTTCGTACAT SEQ ID NO:937	-10	-19.4	59.6	-8.9	-0.1	-4.8
2312	TCACAAAAATCACATATTGA SEQ ID NO:938	-10	-15.6	50.4	-5.1	-0.1	-4.2
2341	AAATTACTGGGAAAATGTAA SEQ ID NO:939	-10	-14.6	48.2	-4.1	-0.1	-4
2486	GTACCAATTTTTAGAAACAT SEQ ID NO:940	-10	-17.3	54.2	-7.3	0	-3.2
2489	CAAGTACCAATTTTTAGAAA SEQ ID NO:941	-10	-16.4	52.1	-6.4	0	-4.4
2490	ACAAGTACCAATTTTTAGAA SEQ ID NO:942	-10	-17.3	54.3	-7.3	0	-4.4
3056	TATTAATTTAATAGCAGCTC SEQ ID NO:943	-10	-17.3	55.5	-7.3	0	-6.3
117	AATATACCACACATGATGCC SEQ ID NO:944	-9.9	-21.8	62.6	-11.9	0	-5.2
451	ATTATTTTTATCAGAGCGCT SEQ ID NO:945	-9.9	-20.9	63.3	-10.2	0	-9.4
452	CATTATTTTTATCAGAGCGC SEQ ID NO:946	-9.9	-20.7	62.6	-10.8	0	-7.2
501	TTCAAGTCTTTGTAGTTGGT SEQ ID NO:947	-9.9	-21.8	68.4	-11.2	-0.5	-3.5
654	GCACCTTCCAATTGTTGGAT SEQ ID NO:948	-9.9	-25.3	71.3	-12.7	-2.7	-8.7
660	GCAAAAGCACCTTCCAATTG SEQ ID NO:949	-9.9	-22.6	63.4	-12.7	0	-5.9
716	TACCTCGCCTTGTGCCAACT SEQ ID NO:950	-9.9	-28.9	77	-18.4	-0.3	-4.6
727	CAACAGAGGGCTACCTCGCC SEQ ID NO:951	-9.9	-28.4	76.3	-15.4	-3.1	-9.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
886	AGAAGCAAAGTAATACTCCA SEQ ID NO:952	-9.9	-19.1	57.8	-9.2	0	-5.6
887	CAGAAGCAAAGTAATACTCC SEQ ID NO:953	-9.9	-19.1	57.8	-9.2	0	-5.6
932	CCAGAAAGATGACGCGATTG SEQ ID NO:954	-9.9	-21.4	60.2	-11	0	-7.9
1693	TAGTTTCTGAATTTCGTCAT SEQ ID NO:955	-9.9	-20	61.9	-10.1	0	-5
1720	TGACTTCTGATGATAAAGTT SEQ ID NO:956	-9.9	-17.9	56.5	-7.1	-0.7	-4
1723	AACTGACTTCTGATGATAAA SEQ ID NO:957	-9.9	-17	53.7	-7.1	0	-2.7
1823	CACCAGCAAGGATGCCTTCA SEQ ID NO:958	-9.9	-27.1	74.4	-15.7	-1.4	-5.9
1890	TCTCTCATGATGATCATGAT SEQ ID NO:959	-9.9	-20.6	63.4	-7.2	-3.5	-11.1
2176	GTTTCGTACATTTTGTATAG SEQ ID NO:960	-9.9	-19.3	60.7	-8.5	-0.8	-4.3
2177	AGTTTCGTACATTTTGTATA SEQ ID NO:961	-9.9	-19.3	60.7	-8.5	-0.8	-4.8
2220	AAGGTTTTAAATACAAAAGG SEQ ID NO:962	-9.9	-14	47.2	-4.1	0	-5.4
2300	CATATTGAGTGGAATAATTA SEQ ID NO:963	-9.9	-16.2	52.4	-6.3	0	-4.1
2468	ATATTGTCTTCTCAGATTGA SEQ ID NO:964	-9.9	-20.1	63.4	-9.7	-0.2	-4.5
2537	CAATTAAATGCACTACTCTT SEQ ID NO:965	-9.9	-18.2	56.2	-8.3	0	-5.5
2695	TCCTACCAATAAAATTTTTC SEQ ID NO:966	-9.9	-17.6	54.4	-7.7	0	-6.7
2776	TTTCGCTTCCTAAATTTCTT SEQ ID NO:967	-9.9	-21.4	63.4	-11.5	0	-4.9
2849	GAATTTAAAGTTTGTGCTAT SEQ ID NO:968	-9.9	-17.4	55.3	-7.5	0	-4.9
31	GTGGGCAATCTGCGGGCTCG SEQ ID NO:969	-9.8	-29.6	79.4	-17.6	-2.2	-8.1
428	GGTGGCTATTGACAGGACTG SEQ ID NO:970	-9.8	-24.5	71.5	-14.7	0	-5.3
432	TGGGGGTGGCTATTGACAGG SEQ ID NO:971	-9.8	-26.4	75.5	-16.6	0	-3.7
500	TCAAGTCTTTGTAGTTGGTG SEQ ID NO:972	-9.8	-21.7	67.9	-11.2	-0.5	-3.5
538	AGATTCGAAGTCATAGCCTT SEQ ID NO:973	-9.8	-22.6	66.5	-12.3	-0.1	-7.6
646	CAATTGTTGGATAACTCTCT SEQ ID NO:974	-9.8	-19.9	60.9	-9.5	-0.3	-5.5
1214	GAATCAAACGCCGGCATCTC SEQ ID NO:975	-9.8	-24.6	66.9	-13.1	0	-11.6
1286	GCAACTCAGTCAGCTCCTCA SEQ ID NO:976	-9.8	-27.4	79.4	-17.6	0	-4.4
1295	CCATCACAGGCAACTCAGTC SEQ ID NO:977	-9.8	-25.5	73.4	-14.8	-0.8	-4
1297	CACCATCACAGGCAACTCAG SEQ ID NO:978	-9.8	-24.8	70.1	-14.1	-0.8	-4.5
1326	TTTCTGTCCAGGAAGTCACT SEQ ID NO:979	-9.8	-24.3	72.4	-14	-0.1	-5.5
1329	GTGTTTCTGTCCAGGAAGTC SEQ ID NO:980	-9.8	-24.9	75.7	-14.6	-0.1	-5.5
1603	TTGCATGGAGATCCGATCAT SEQ ID NO:981	-9.8	-23.9	68	-13.2	-0.7	-7.5

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1771	TGCCCCTTCAAGACAAGTAG SEQ ID NO:982	-9.8	-24.9	69.8	-15.1	0	-3
1909	ACACTTGGCATAAGTGTGAT SEQ ID NO:983	-9.8	-21.8	65.1	-8.2	-3.8	-10.4
1910	GACACTTGGCATAAGTGTGA SEQ ID NO:984	-9.8	-22.4	66.4	-8.2	-4.4	-11.2
2307	AAAATCACATATTGAGTGGA SEQ ID NO:985	-9.8	-17.3	54.3	-6.9	-0.3	-4.7
2520	CTTTCACTGGTCTGAATGAA SEQ ID NO:986	-9.8	-20.8	62.7	-10.4	-0.3	-4.4
2777	ATTTCGCTTCCTAAATTTCT SEQ ID NO:987	-9.8	-21.3	63.1	-11.5	0	-4.9
2945	TTTTAGGAGATGAAAACACA SEQ ID NO:988	-9.8	-16.7	52.9	-6.9	0	-3
53	GGGGGTGCACACACGAGCTT SEQ ID NO:989	-9.7	-28.7	78.7	-16.6	-2.4	-9.8
116	ATATACCACACATGATGCCG SEQ ID NO:990	-9.7	-23.3	64.9	-13.6	0	-5.2
656	AAGCACCTTCCAATTGTTGG SEQ ID NO:991	-9.7	-24	68.1	-12.7	-1.5	-7.1
870	TCCACTGCTTTTTCTTCCAC SEQ ID NO:992	-9.7	-26	75.2	-16.3	0	-3.6
1081	CTGCATAAATGAACTGAAGT SEQ ID NO:993	-9.7	-17.8	54.8	-8.1	0	-4.9
1153	AGTATAGTCATCAAAGTTGA SEQ ID NO:994	-9.7	-18.5	59	-8.8	0	-5.7
1167	CCACCCAAATTCACAGTATA SEQ ID NO:995	-9.7	-22.9	64.6	-13.2	0	-3.1
1291	CACAGGCAACTCAGTCAGCT SEQ ID NO:996	-9.7	-25.8	74.7	-15.2	-0.8	-5.7
1492	ATGAACTCCACAATCTGTCT SEQ ID NO:997	-9.7	-22.1	65.2	-12.4	0	-2.6
1497	TTAATATGAACTCCACAATC SEQ ID NO:998	-9.7	-17.5	54.5	-7.8	0	-2.7
2186	TAATCATACAGTTTCGTACA SEQ ID NO:999	-9.7	-19.1	59.1	-8.9	-0.1	-4.8
2316	AACTTCACAAAAATCACATA SEQ ID NO:1000	-9.7	-15.4	49.8	-5.7	0	-1.1
2317	TAACTTCACAAAAATCACAT SEQ ID NO:1001	-9.7	-15.4	49.8	-5.7	0	-1.1
2587	TCCCTAACTGTCCAAGTATG SEQ ID NO:1002	-9.7	-23.9	68.3	-13.5	-0.5	-3.2
2861	CCAAAGCAGCTTGAATTTAA SEQ ID NO:1003	-9.7	-19.7	58.3	-9.4	0	-8.4
122	AAGCAAATATACCACACATG SEQ ID NO:1004	-9.6	-18.5	55.6	-8.9	0	-4.7
192	AGTCTCTGAAGGCCTTTGAT SEQ ID NO:1005	-9.6	-24.4	71.9	-13.4	-0.1	-10.8
461	CGATAAATTCATTATTTTTA SEQ ID NO:1006	-9.6	-14.8	49.2	-4.5	-0.5	-4.9
464	TAACGATAAATTCATTATTT SEQ ID NO:1007	-9.6	-14.1	47.5	-4.5	0	-3.6
586	GTCATACATATACTTAACGA SEQ ID NO:1008	-9.6	-18.1	56.2	-8.5	0	-3.5
641	GTTGGATAACTCTCTCCACC SEQ ID NO:1009	-9.6	-25.1	72.5	-14.2	-1.2	-4.7
706	TGTGCCAACTGCTTGCCCGG SEQ ID NO:1010	-9.6	-30.7	79.6	-20.1	-0.9	-7
1018	AGCTCGTCCGGGGTGATCTC SEQ ID NO:1011	-9.6	-29.4	82.1	-19.8	0	-6.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1119	GTGTTCACGACAGACTCTGG SEQ ID NO:1012	-9.6	-24.3	71.1	-13.8	-0.7	-6.8
1504	ACCAGCATTAATATGAACTC SEQ ID NO:1013	-9.6	-19.6	59.1	-10	0.3	-4.2
1622	TGATCTCTTTGCGTCTTTCT SEQ ID NO:1015	-9.6	-24	72.1	-14.4	0	-4.9
1634	TCAATCCAAGCATGATCTCT SEQ ID NO:1015	-9.6	-22.5	66.1	-12.9	0	-4.9
1951	AGGCCGCCCCTGCCGAGCAA SEQ ID NO:1016	-9.6	-35.5	85.7	-23.5	-2.4	-9
2064	TGTAAAGGGATCACGCTGAG SEQ ID NO:1017	-9.6	-21.9	63.7	-11.8	-0.1	-5.3
2403	TAATAGCTAGAATCTTTCTG SEQ ID NO:1018	-9.6	-17.8	56.8	-7.3	-0.7	-6.8
2405	AATAATAGCTAGAATCTTTC SEQ ID NO:1019	-9.6	-16.2	53	-6.6	0	-6
2507	GAATGAAGTATGGTGAAACA SEQ ID NO:1020	-9.6	-17.2	53.8	-6.6	-0.9	-3.9
6	CGGGGTGGCGCCGACACGAC SEQ ID NO:1021	-9.5	-31.3	77.8	-19.5	-1.6	-12.5
128	TTAAGTAAGCAAATATACCA SEQ ID NO:1022	-9.5	-16.7	52.7	-7.2	0	-4.1
129	TTTAAGTAAGCAAATATACC SEQ ID NO:1023	-9.5	-16.1	51.7	-6.6	0	-4.1
170	GGGTCTCCAGGATTTCTCGT SEQ ID NO:1024	-9.5	-27.7	80.2	-17.5	-0.4	-4.8
298	TTTTCCTTTCTTCTTAATAA SEQ ID NO:1025	-9.5	-18.6	58.6	-9.1	0	-2.3
457	AAATTCATTATTTTTATCAG SEQ ID NO:1026	-9.5	-14.8	50	-5.3	0	-3.1
554	TCTCTGTGTCTGTTTCAGAT SEQ ID NO:1027	-9.5	-23.4	73.3	-12.4	-1.4	-6.3
618	GTAGTAAAGCTGGTATCTTG SEQ ID NO:1028	-9.5	-20.6	63.8	-11.1	0	-5.1
876	TAATACTCCACTGCTTTTTC SEQ ID NO:1029	-9.5	-21.5	64.7	-12	0	-3.6
1005	TGATCTCCTGCAGTTCGTTT SEQ ID NO:1030	-9.5	-25.6	74.7	-15.6	0	-8.2
1121	TTGTGTTCACGACAGACTCT SEQ ID NO:1031	-9.5	-23.2	68.8	-12.8	-0.7	-6.4
1231	TGTTCCACAAGCAATAAGAA SEQ ID NO:1032	-9.5	-19.3	57.8	-9.8	0	-4.8
1328	TGTTTCTGTCCAGGAAGTCA SEQ ID NO:1033	-9.5	-24.4	73.1	-14.4	-0.1	-5.5
1649	AATCAGGCAGCCGTTTCAAT SEQ ID NO:1034	-9.5	-24.5	69.1	-15	0.5	-8.2
1814	GGATGCCTTCAGAGTGCATA SEQ ID NO:1035	-9.5	-25.7	74.4	-13.4	-2.8	-6.9
1960	AATTACCACAGGCCGCCCCT SEQ ID NO:1036	-9.5	-31.4	79	-21.2	-0.5	-7.7
2362	CCATTATTCAAAGTCCTCCA SEQ ID NO:1037	-9.5	-23.9	68	-14.4	0	-1.6
2488	AAGTACCAATTTTTAGAAAC SEQ ID NO:1038	-9.5	-15.9	51.3	-6.4	0	-4.4
186	TGAAGGCCTTTGATTAGGGT SEQ ID NO:1039	-9.4	-24	69.7	-13.2	-0.3	-10.8
305	CCTTAACTTTTCCTTTCTTC SEQ ID NO:1040	-9.4	-22.7	67.8	-13.3	0	-2.2
657	AAAGCACCTTCCAATTGTTG SEQ ID NO:1041	-9.4	-22.1	63.6	-12.7	0	-7.1

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
661	TGCAAAAGCACCTTCCAATT SEQ ID NO:1042	-9.4	-22.6	63.4	-12.7	-0.1	-4.8
662	GTGCAAAAGCACCTTCCAAT SEQ ID NO:1043	-9.4	-23.7	66	-12.7	-1.6	-7.8
879	AAGTAATACTCCACTGCTTT SEQ ID NO:1044	-9.4	-21.4	63.8	-12	0	-5.6
973	AGAAAGACGTCCATCCACTA SEQ ID NO:1045	-9.4	-23	65.3	-13.1	0	-8.2
1038	TCCATCTGGAGTGTTTGCAC SEQ ID NO:1046	-9.4	-25.5	75	-14.4	-1.7	-10
1120	TGTGTTCACGACAGACTCTG SEQ ID NO:1047	-9.4	-23.1	68.3	-12.8	-0.7	-6.9
1215	AGAATCAAACGCCGGCATCT SEQ ID NO:1048	-9.4	-24.2	65.8	-13.1	0	-11.6
1489	AACTCCACAATCTGTCTCCC SEQ ID NO:1049	-9.4	-25.9	72.8	-16.5	0	-2.6
1692	AGTTTCTGAATTTCGTCATC SEQ ID NO:1050	-9.4	-20.7	64	-11.3	0	-5
1717	CTTCTGATGATAAAGTTCTG SEQ ID NO:1051	-9.4	-18.4	57.9	-9	0	-2.7
1819	AGCAAGGATGCCTTCAGAGT SEQ ID NO:1052	-9.4	-25.3	73.3	-13.7	-2.2	-6.7
1966	ATCACAAATTACCACAGGCC SEQ ID NO:1053	-9.4	-23.2	65.5	-13.8	0	-6.4
2760	TCTTCCACCTACAGATAATA SEQ ID NO:1054	-9.4	-21.5	63.6	-12.1	0	-2.2
2923	GTAGTAGGATACCCAACATG SEQ ID NO:1055	-9.4	-22.4	65.4	-12.1	-0.8	-6.1
173	TTAGGGTCTCCAGGATTTCT SEQ ID NO:1056	-9.3	-25.1	75	-14.6	-1.1	-5
303	TTAACTTTTCCTTTCTTCTT SEQ ID NO:1057	-9.3	-20.8	64.3	-11.5	0	-2
399	TGTGTTGCCCAACGGGTATG SEQ ID NO:1058	-9.3	-26.6	72.9	-16	-1.2	-7.7
463	AACGATAAATTCATTATTTT SEQ ID NO:1059	-9.3	-14.5	48.3	-4.5	-0.5	-3.7
659	CAAAAGCACCTTCCAATTGT SEQ ID NO:1060	-9.3	-22	62.5	-12.7	0	-7.1
704	TGCCAACTGCTTGCCCGGGA SEQ ID NO:1061	-9.3	-31.3	80.1	-20.1	-0.9	-11.9
726	AACAGAGGGCTACCTCGCCT SEQ ID NO:1062	-9.3	-28.6	77.1	-15.4	-3.9	-9.6
1033	CTGGAGTGTTTGCACAGCTC SEQ ID NO:1063	-9.3	-25.8	76.5	-14.6	-1.9	-8.4
1123	CATTGTGTTCACGACAGACT SEQ ID NO:1064	-9.3	-22.6	66.4	-12.8	-0.2	-6.4
1301	GTTCCACCATCACAGGCAAC SEQ ID NO:1065	-9.3	-26.5	74	-17.2	0	-4
1599	ATGGAGATCCGATCATCACA SEQ ID NO:1066	-9.3	-23.3	66.9	-13.3	-0.4	-7.2
1633	CAATCCAAGCATGATCTCTT SEQ ID NO:1067	-9.3	-22.2	65	-12.9	0	-4.9
1752	GCATAATGATAGCCTCGTCC SEQ ID NO:1068	-9.3	-25.3	71	-16	0	-3.5
1948	CCGCCCCTGCCGAGCAACCA SEQ ID NO:1069	-9.3	-35.4	83.6	-25.2	-0.7	-7.1
1959	ATTACCACAGGCCGCCCCTG SEQ ID NO:1070	-9.3	-32.1	81.1	-20.2	-2.6	-8.4
2063	GTAAAGGGATCACGCTGAGA SEQ ID NO:1071	-9.3	-22.5	65.1	-12.7	-0.1	-5.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2483	CCAATTTTTAGAAACATATT SEQ ID NO:1072	-9.3	-16	51.3	-6.7	0	-2.9
2582	AACTGTCCAAGTATGAGCAT SEQ ID NO:1073	-9.3	-22	65	-12	-0.5	-5
2969	CAGATACAAGGAAATAAAAA SEQ ID NO:1074	-9.3	-12.5	43.9	-3.2	0	-1.3
3043	GCAGCTCTGTGTTGTGATTT SEQ ID NO:1075	-9.3	-25	75.4	-15.7	0	-4.8
43	ACACGAGCTTCGGTGGGCAA SEQ ID NO:1076	-9.2	-27.1	73.6	-16.4	-1.4	-7.3
51	GGGTGCACACACGAGCTTCG SEQ ID NO:1077	-9.2	-27.5	75.1	-15.9	-2.4	-11.8
204	CCTCTGTACTCCAGTCTCTG SEQ ID NO:1078	-9.2	-27.1	79.7	-17	-0.8	-4.1
394	TGCCCAACGGGTATGAGCTA SEQ ID NO:1079	-9.2	-27.1	73.3	-16.6	-1.2	-7.6
497	AGTCTTTGTAGTTGGTGATG SEQ ID NO:1080	-9.2	-21.9	68.7	-12.7	0	-2.3
599	GACTTTCCCGATTGTCATAC SEQ ID NO:1081	-9.2	-24	68.8	-14.2	-0.3	-4.3
881	CAAAGTAATACTCCACTGCT SEQ ID NO:1082	-9.2	-21.2	62.2	-12	0	-5.6
978	TGGATAGAAAGACGTCCATC SEQ ID NO:1083	-9.2	-21	61.8	-10.7	-1	-8.6
1292	TCACAGGCAACTCAGTCAGC SEQ ID NO:1084	-9.2	-25.3	74.5	-15.2	-0.8	-5.8
1457	TGCCAACTGTGTTTGTGATC SEQ ID NO:1085	-9.2	-23.7	69.8	-14.5	0	-4.2
1764	TCAAGACAAGTAGCATAATG SEQ ID NO:1086	-9.2	-17.6	55.2	-8.4	0	-4.1
1972	CTCCTTATCACAAATTACCA SEQ ID NO:1087	-9.2	-21.3	62.1	-12.1	0	-3.2
2299	ATATTGAGTGGAATAATTAT SEQ ID NO:1088	-9.2	-15.5	51.1	-6.3	0	-5.9
2308	AAAAATCACATATTGAGTGG SEQ ID NO:1089	-9.2	-16	51.4	-5.9	-0.7	-4.6
2353	AAAGTCCTCCACAAATTACT SEQ ID NO:1090	-9.2	-20.6	60.4	-11.4	0	-3.2
2460	TTCTCAGATTGAAGTGGAGG SEQ ID NO:1091	-9.2	-21.3	65.1	-12.1	0	-4.3
2580	CTGTCCAAGTATGAGCATAC SEQ ID NO:1092	-9.2	-22.4	66.6	-12.5	-0.3	-8.3
2624	AATAAATCACATCTTCTCTT SEQ ID NO:1093	-9.2	-17.7	56.1	-8.5	0	-1.2
2679	TTTCAGTTTTAAGTTTTACA SEQ ID NO:1094	-9.2	-17.9	58	-8.7	0	-2.6
2965	TACAAGGAAATAAAAAACAC SEQ ID NO:1095	-9.2	-11.6	42.3	-2.4	0	-1.2
97	GGAGACACGGCCCGCGAGGC SEQ ID NO:1096	-9.1	-32.3	81.1	-20.6	-2.1	-13
119	CAAATATACCACACATGATG SEQ ID NO:1097	-9.1	-18	54.7	-8.9	0	-5.2
127	TAAGTAAGCAAATATACCAC SEQ ID NO:1098	-9.1	-16.8	52.8	-7.7	0	-4.1
244	ATCATTGCCTCCATCAAATC SEQ ID NO:1099	-9.1	-23.1	66.6	-14	0	-3.7
629	TCTCCACCAAGGTAGTAAAG SEQ ID NO:1100	-9.1	-22.2	65	-12.6	-0.2	-4.9
640	TTGGATAACTCTCTCCACCA SEQ ID NO:1101	-9.1	-24.6	70.3	-14.2	-1.2	-4.9

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
648	TCCAATTGTTGGATAACTCT SEQ ID NO:1102	-9.1	-21	62.7	-9.5	-2.4	-7.7
768	ATGTGATCAGTAGAAAGTTT SEQ ID NO:1103	-9.1	-18.4	58.5	-9.3	0	-6.6
1001	CTCCTGCAGTTCGTTTAATT SEQ ID NO:1104	-9.1	-23.7	69.2	-14.1	0	-8.2
1766	CTTCAAGACAAGTAGCATAA SEQ ID NO:1105	-9.1	-18.6	57.5	-9.5	0	-4.1
1914	TTCTGACACTTGGCATAAGT SEQ ID NO:1106	-9.1	-22	65.8	-11.9	-0.9	-4.8
2123	GATTCCGTGGGAAATCAACA SEQ ID NO:1107	-9.1	-22	62.6	-11.4	-1.4	-6.5
2491	AACAAGTACCAATTTTTAGA SEQ ID NO:1108	-9.1	-17.3	54.3	-8.2	0	-3.6
2531	AATGCACTACTCTTTCACTG SEQ ID NO:1109	-9.1	-21.4	64.4	-12.3	0	-5.5
2950	AACACTTTTAGGAGATGAAA SEQ ID NO:1110	-9.1	-16.9	53.5	-7.8	0	-2.4
2951	AAACACTTTTAGGAGATGAA SEQ ID NO:1111	-9.1	-16.9	53.5	-7.8	0	-2.4
2952	AAAACACTTTTAGGAGATGA SEQ ID NO:1112	-9.1	-16.9	53.5	-7.8	0	-2.7
118	AAATATACCACACATGATGC SEQ ID NO:1113	-9	-19.1	57.2	-10.1	0	-5.2
125	AGTAAGCAAATATACCACAC SEQ ID NO:1115	-9	-18.7	56.8	-9.7	0	-3.3
245	TATCATTGCCTCCATCAAAT SEQ ID NO:1115	-9	-22.4	64.6	-13.4	0	-3.7
587	TGTCATACATATACTTAACG SEQ ID NO:1116	-9	-17.5	54.9	-8.5	0	-3
611	AGCTGGTATCTTGACTTTCC SEQ ID NO:1117	-9	-24.5	73.1	-15.5	0	-4.3
816	AGATTGCAGCTTCCTTTCTT SEQ ID NO:1118	-9	-24.9	73.8	-15.9	0	-5.2
937	ATCTTCCAGAAAGATGACGC SEQ ID NO:1119	-9	-21.7	63	-11	-1.7	-6.7
1101	GGCTGCTCAAATATTTCCTT SEQ ID NO:1120	-9	-23.6	68.3	-14.6	0	-6.1
1448	TGTTTGTGATCCCCACAGTT SEQ ID NO:1121	-9	-26.5	75.4	-15.4	-2.1	-7.1
1496	TAATATGAACTCCACAATCT SEQ ID NO:1122	-9	-18.3	56	-9.3	0	-2.7
1500	GCATTAATATGAACTCCACA SEQ ID NO:1123	-9	-20.3	60.1	-10.6	-0.4	-5.2
1818	GCAAGGATGCCTTCAGAGTG SEQ ID NO:1124	-9	-25.3	72.8	-14.8	-1.4	-5.5
1875	ATGATCACAGGCATCAATTT SEQ ID NO:1125	-9	-20.9	62.7	-11.2	-0.4	-6.8
1958	TTACCACAGGCCGCCCCTGC SEQ ID NO:1126	-9	-33.9	85.1	-22.1	-2.8	-8.7
2346	TCCACAAATTACTGGGAAAA SEQ ID NO:1127	-9	-18.4	55.1	-8.8	-0.3	-5.9
2676	CAGTTTTAAGTTTTACAGTT SEQ ID NO:1128	-9	-18.6	59.7	-9.6	0	-2.6
2944	TTTAGGAGATGAAAACACAA SEQ ID NO:1129	-9	-15.9	51	-6.9	0	-2.5
3044	AGCAGCTCTGTGTTGTGATT SEQ ID NO:1130	-9	-24.9	75.3	-15.9	0	-5.6
217	AGCAGAATCATATCCTCTGT SEQ ID NO:1131	-8.9	-23	68.6	-12.9	-1.1	-4.9

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
302	TAACTTTTCCTTTCTTCTTA SEQ ID NO:1132	-8.9	-20.4	63.3	-11.5	0	-1
608	TGGTATCTTGACTTTCCCGA SEQ ID NO:1133	-8.9	-25.2	71.5	-16.3	0	-3.2
884	AAGCAAAGTAATACTCCACT SEQ ID NO:1134	-8.9	-19.6	58.7	-10.7	0	-5.6
1079	GCATAAATGAACTGAAGTTG SEQ ID NO:1135	-8.9	-17	53.3	-8.1	0	-5.7
1080	TGCATAAATGAACTGAAGTT SEQ ID NO:1136	-8.9	-17	53.3	-8.1	0	-5.7
1082	TCTGCATAAATGAACTGAAG SEQ ID NO:1137	-8.9	-17	53.3	-8.1	0	-4.9
1102	TGGCTGCTCAAATATTTCCT SEQ ID NO:1138	-8.9	-23.5	67.9	-14.6	0	-6.1
1103	CTGGCTGCTCAAATATTTCC SEQ ID NO:1139	-8.9	-23.5	67.9	-14.6	0	-6.1
1337	AGACTGGTGTGTTTCTGTCC SEQ ID NO:1140	-8.9	-25.6	77.4	-15.8	-0.7	-4
1861	CAATTTATCCACCAAAGCCA SEQ ID NO:1141	-8.9	-23	63.9	-14.1	0	-3.2
2298	TATTGAGTGGAATAATTATA SEQ ID NO:1142	-8.9	-15.2	50.5	-6.3	0	-6.2
2336	ACTGGGAAAATGTAAGAGGT SEQ ID NO:1143	-8.9	-19.2	58.2	-10.3	0	-2.2
2962	AAGGAAATAAAAAACACTTT SEQ ID NO:1144	-8.9	-12.1	43.3	-3.2	0	-2.8
37	GCTTCGGTGGGCAATCTGCG SEQ ID NO:1145	-8.8	-28.5	77.3	-17.5	-2.2	-6.6
50	GGTGCACACACGAGCTTCGG SEQ ID NO:1146	-8.8	-27.5	75.1	-16.2	-2.4	-12.3
151	TCTCGTTCGAGGAACATGGT SEQ ID NO:1147	-8.8	-24	68.9	-13.3	-1.9	-9.1
251	AATCTTTATCATTGCCTCCA SEQ ID NO:1148	-8.8	-23.5	68.2	-14.7	0	-3
307	TGCCTTAACTTTTCCTTTCT SEQ ID NO:1149	-8.8	-24	70	-15.2	0	-3
465	ATAACGATAAATTCATTATT SEQ ID NO:1150	-8.8	-14	47.3	-4.5	-0.5	-3.6
502	TTTCAAGTCTTTGTAGTTGG SEQ ID NO:1151	-8.8	-20.7	65.2	-11.2	-0.5	-3.5
712	TCGCCTTGTGCCAACTGCTT SEQ ID NO:1152	-8.8	-28.9	77.9	-19.1	-0.9	-6.1
1290	ACAGGCAACTCAGTCAGCTC SEQ ID NO:1153	-8.8	-25.5	75.4	-15.8	-0.8	-5.8
1332	GGTGTGTTTCTGTCCAGGAA SEQ ID NO:1154	-8.8	-25.7	76.1	-16.9	0	-5.5
1726	CAGAACTGACTTCTGATGAT SEQ ID NO:1155	-8.8	-20	60.7	-9	-2.2	-6.1
2132	ATTTGGCAAGATTCCGTGGG SEQ ID NO:1156	-8.8	-24.7	69.5	-15.4	-0.1	-4.2
2519	TTTCACTGGTCTGAATGAAG SEQ ID NO:1157	-8.8	-19.9	61	-10.4	-0.5	-4.6
2663	TACAGTTTGATTTAAAAACA SEQ ID NO:1158	-8.8	-14.6	48.7	-4.1	-1.7	-6.3
3001	CATTCAGCAGTCATTTAAAA SEQ ID NO:1159	-8.8	-18.5	57.4	-9.7	0	-5
458	TAAATTCATTATTTTTATCA SEQ ID NO:1160	-8.7	-14.5	49.3	-5.3	-0.2	-3.1
471	TTGTGAATAACGATAAATTC SEQ ID NO:1161	-8.7	-14.6	48.4	-5.3	-0.3	-3.9

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
526	ATAGCCTTTGCTTTCCAAAA SEQ ID NO:1162	-8.7	-22.5	64.6	-12.4	-1.3	-5.9
658	AAAAGCACCTTCCAATTGTT SEQ ID NO:1163	-8.7	-21.4	61.7	-12.7	0	-7.1
1160	AATTCACAGTATAGTCATCA SEQ ID NO:1164	-8.7	-19.4	61.1	-10.7	0	-2.7
1230	GTTCCACAAGCAATAAGAAT SEQ ID NO:1165	-8.7	-19.3	57.8	-10.6	0	-4.1
1539	GTATAAGCCTTTGTACTGGC SEQ ID NO:1166	-8.7	-23.8	70.2	-13.5	-1.5	-7.8
1579	CATCATAAGGGCAAACATCA SEQ ID NO:1167	-8.7	-20.3	60	-11.6	0	-4
1716	TTCTGATGATAAAGTTCTGT SEQ ID NO:1168	-8.7	-18.7	59	-10	0	-2.7
1775	TCAGTGCCCCTTCAAGACAA SEQ ID NO:1169	-8.7	-26.3	72.7	-17.6	0	-3.8
1865	GCATCAATTTATCCACCAAA SEQ ID NO:1170	-8.7	-21.4	61.6	-12.7	0	-3.4
1884	ATGATGATCATGATCACAGG SEQ ID NO:1171	-8.7	-20.1	61.2	-8.4	-1	-14.2
3048	TAATAGCAGCTCTGTGTTGT SEQ ID NO:1172	-8.7	-22.9	69.7	-14.2	0	-6.1
79	GCCAGGGGCGAGTGGCTGGC SEQ ID NO:1173	-8.6	-33.4	89.4	-21.4	-3.4	-10
133	GTAGTTTAAGTAAGCAAATA SEQ ID NO:1174	-8.6	-16.3	53.1	-7.7	0	-4.1
140	GAACATGGTAGTTTAAGTAA SEQ ID NO:1175	-8.6	-17.5	55.7	-8.9	0	-5.2
243	TCATTGCCTCCATCAAATCC SEQ ID NO:1176	-8.6	-25.1	70.2	-16.5	0	-3.7
479	TGATTCCATTGTGAATAACG SEQ ID NO:1177	-8.6	-19	57	-9.7	-0.5	-6.1
505	CTTTTTCAAGTCTTTGTAGT SEQ ID NO:1178	-8.6	-20.5	65	-11.2	-0.5	-3.2
517	GCTTTCCAAAAACTTTTTCA SEQ ID NO:1179	-8.6	-19.8	59.3	-11.2	0	-4.9
663	AGTGCAAAAGCACCTTCCAA SEQ ID NO:1180	-8.6	-23.7	66.2	-12.7	-2.4	-9
767	TGTGATCAGTAGAAAGTTTA SEQ ID NO:1181	-8.6	-18.1	57.9	-9.5	0	-6.6
880	AAAGTAATACTCCACTGCTT SEQ ID NO:1182	-8.6	-20.6	61.4	-12	0	-5.6
1122	ATTGTGTTCACGACAGACTC SEQ ID NO:1183	-8.6	-22.3	66.8	-12.8	-0.7	-6.4
1169	AACCACCCAAATTCACAGTA SEQ ID NO:1184	-8.6	-22.7	63.7	-14.1	0	-3.1
1499	CATTAATATGAACTCCACAA SEQ ID NO:1185	-8.6	-17.8	54.5	-9.2	0	-5.2
1510	CTCAGGACCAGCATTAATAT SEQ ID NO:1186	-8.6	-22	64.6	-13.4	0	-4.2
1824	TCACCAGCAAGGATGCCTTC SEQ ID NO:1187	-8.6	-26.8	75	-16	-2.2	-5.9
1952	CAGGCCGCCCCTGCCGAGCA SEQ ID NO:1188	-8.6	-36.9	88.9	-25.9	-2.4	-8.8
2467	TATTGTCTTCTCAGATTGAA SEQ ID NO:1189	-8.6	-19.4	61.2	-10.8	0.2	-4.7
2501	AGTATGGTGAAACAAGTACC SEQ ID NO:1190	-8.6	-19.8	59.9	-10.2	-0.9	-5.3
2558	TGCCACTGGCTTTAGATACT SEQ ID NO:1191	-8.6	-24.8	71.5	-14.1	-2.1	-9.7

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2779	ATATTTCGCTTCCTAAATTT SEQ ID NO:1192	-8.6	-19.7	59.3	-11.1	0	-4.5
2782	GTAATATTTCGCTTCCTAAA SEQ ID NO:1193	-8.6	-19.7	59.1	-11.1	0	-4.2
2848	AATTTAAAGTTTGTGCTATA SEQ ID NO:1194	-8.6	-16.5	53.5	-7.9	0	-4.9
2949	ACACTTTTAGGAGATGAAAA SEQ ID NO:1195	-8.6	-16.9	53.5	-8.3	0	-3
131	AGTTTAAGTAAGCAAATATA SEQ ID NO:1196	-8.5	-15.1	50.3	-6.6	0	-4.1
219	CCAGCAGAATCATATCCTCT SEQ ID NO:1197	-8.5	-24.5	70.3	-16	0	-4.1
504	TTTTTCAAGTCTTTGTAGTT SEQ ID NO:1198	-8.5	-19.7	63.3	-11.2	0.1	-2.9
561	GCAATTGTCTCTGTGTCTGT SEQ ID NO:1199	-8.5	-24.6	74.9	-16.1	0	-6.8
571	AACGAGCTTGGCAATTGTCT SEQ ID NO:1200	-8.5	-23.3	66.9	-14.3	0.1	-8.3
917	GATTGGTGTGTTCTATGACA SEQ ID NO:1201	-8.5	-22.1	67.5	-13.6	0	-3.2
998	CTGCAGTTCGTTTAATTCGA SEQ ID NO:1202	-8.5	-22.2	65.1	-13	-0.5	-7.9
1034	TCTGGAGTGTTTGCACAGCT SEQ ID NO:1203	-8.5	-25.8	76.5	-14.6	-2.7	-9.1
1421	CTCTCTCCTTACAGTAACGA SEQ ID NO:1204	-8.5	-23.3	68.1	-14.8	0	-4.7
1691	GTTTCTGAATTTCGTCATCC SEQ ID NO:1205	-8.5	-22.7	67.7	-14.2	0	-5
1762	AAGACAAGTAGCATAATGAT SEQ ID NO:1206	-8.5	-17.1	54	-8.6	0	-4.1
2122	ATTCCGTGGGAAATCAACAT SEQ ID NO:1207	-8.5	-21.4	61.4	-11.4	-1.4	-6.5
2264	AAGGATTTACTAAAAAAAGG SEQ ID NO:1208	-8.5	-12.8	44.8	-4.3	0	-2.4
2297	ATTGAGTGGAATAATTATAA SEQ ID NO:1209	-8.5	-14.8	49.4	-6.3	0	-6.2
2313	TTCACAAAAATCACATATTG SEQ ID NO:1210	-8.5	-15.1	49.5	-6.6	0	-4
2472	AAACATATTGTCTTCTCAGA SEQ ID NO:1211	-8.5	-18.9	59.3	-9.9	-0.2	-3.1
2581	ACTGTCCAAGTATGAGCATA SEQ ID NO:1212	-8.5	-22.4	66.6	-13.9	0	-4.9
2596	GCAAACCCTTCCCTAACTGT SEQ ID NO:1213	-8.5	-26.9	72.1	-18.4	0	-3.4
2696	ATCCTACCAATAAAATTTTT SEQ ID NO:1215	-8.5	-17.2	53.3	-8.7	0	-6.7
2860	CAAAGCAGCTTGAATTTAAA SEQ ID NO:1215	-8.5	-17	53	-7.9	0	-8.4
2940	GGAGATGAAAACACAAAGTA SEQ ID NO:1216	-8.5	-16.2	51.4	-7.7	0	-2.9
27	GCAATCTGCGGGCTCGGGGG SEQ ID NO:1217	-8.4	-30.8	81.1	-20.9	-1.4	-8.1
141	GGAACATGGTAGTTTAAGTA SEQ ID NO:1218	-8.4	-19.4	60.3	-11	0	-5.2
193	CAGTCTCTGAAGGCCTTTGA SEQ ID NO:1219	-8.4	-25.1	73.1	-15.2	-0.1	-10.9
423	CTATTGACAGGACTGGGTTC SEQ ID NO:1220	-8.4	-23.2	69.3	-14.8	0	-5.8
624	ACCAAGGTAGTAAAGCTGGT SEQ ID NO:1221	-8.4	-22.9	66.9	-13.8	-0.4	-5.1

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
766	GTGATCAGTAGAAAGTTTAT SEQ ID NO:1222	-8.4	-18.1	58	-9.7	0	-6.6
801	TTCTTGTCTTTGCCTGTTCT SEQ ID NO:1223	-8.4	-25.5	76.9	-17.1	0	-3
809	AGCTTCCTTTCTTGTCTTTG SEQ ID NO:1224	-8.4	-24.4	74.1	-16	0	-4.3
1124	TCATTGTGTTCACGACAGAC SEQ ID NO:1225	-8.4	-22.1	66	-12.8	-0.7	-5.7
1517	CACCAATCTCAGGACCAGCA SEQ ID NO:1226	-8.4	-26.5	73.3	-18.1	0	-4.1
1637	GTTTCAATCCAAGCATGATC SEQ ID NO:1227	-8.4	-21.7	64.6	-13.3	0	-4.8
1699	TGTTGCTAGTTTCTGAATTT SEQ ID NO:1228	-8.4	-20.5	63.8	-12.1	0	-4.7
1868	CAGGCATCAATTTATCCACC SEQ ID NO:1229	-8.4	-24	68.3	-15.6	0	-4
2003	TTCTTTTTGTGTTCTTAATG SEQ ID NO:1230	-8.4	-18.7	60	-10.3	0	-2.3
2335	CTGGGAAAATGTAAGAGGTA SEQ ID NO:1231	-8.4	-18.7	57.2	-10.3	0	-1.5
2347	CTCCACAAATTACTGGGAAA SEQ ID NO:1232	-8.4	-20	58.6	-11	-0.3	-5.9
2532	AAATGCACTACTCTTTCACT SEQ ID NO:1233	-8.4	-20.7	62.4	-12.3	0	-5.5
2536	AATTAAATGCACTACTCTTT SEQ ID NO:1234	-8.4	-17.6	55.2	-9.2	0	-5.5
2539	TCCAATTAAATGCACTACTC SEQ ID NO:1235	-8.4	-19.6	58.9	-11.2	0	-5.5
2625	AAATAAATCACATCTTCTCT SEQ ID NO:1236	-8.4	-16.9	53.9	-8.5	0	-1.2
3045	TAGCAGCTCTGTGTTGTGAT SEQ ID NO:1237	-8.4	-24.5	74.2	-16.1	0	-6.1
377	CTATTCCAAGGTGTACATCA SEQ ID NO:1238	-8.3	-22.4	66.6	-13.6	0	-7.9
470	TGTGAATAACGATAAATTCA SEQ ID NO:1239	-8.3	-15.2	49.3	-5.3	-1.6	-5.8
542	TTTCAGATTCGAAGTCATAG SEQ ID NO:1240	-8.3	-19.1	59.5	-10.8	0.6	-6.8
834	GTGCTGTCCACACGAGAGAG SEQ ID NO:1241	-8.3	-25.9	73.8	-16.4	-1.1	-5.3
888	TCAGAAGCAAAGTAATACTC SEQ ID NO:1242	-8.3	-17.5	55.3	-9.2	0	-5.6
924	ATGACGCGATTGGTGTGTTC SEQ ID NO:1243	-8.3	-24.2	69.5	-15	-0.8	-7.9
943	ATCATCATCTTCCAGAAAGA SEQ ID NO:1244	-8.3	-20.5	62	-11	-1.1	-4
1447	GTTTGTGATCCCCACAGTTA SEQ ID NO:1245	-8.3	-26.2	75	-15.8	-2.1	-7.1
1606	TTCTTGCATGGAGATCCGAT SEQ ID NO:1246	-8.3	-24.2	69.2	-15.4	-0.2	-6.4
1621	GATCTCTTTGCGTCTTTCTT SEQ ID NO:1247	-8.3	-24.1	72.7	-15.8	0	-4.1
1755	GTAGCATAATGATAGCCTCG SEQ ID NO:1248	-8.3	-22.6	65.6	-13.8	-0.1	-4.1
1756	AGTAGCATAATGATAGCCTC SEQ ID NO:1249	-8.3	-21.8	65.6	-13	-0.1	-4.1
2306	AAATCACATATTGAGTGGAA SEQ ID NO:1250	-8.3	-17.3	54.3	-8.1	-0.7	-4.7
2618	TCACATCTTCTCTTAAAACT SEQ ID NO:1251	-8.3	-18.8	58.6	-10.5	0	-2.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2775	TTCGCTTCCTAAATTTCTTC SEQ ID NO:1252	-8.3	-21.7	64.5	-13.4	0	-4.9
2946	CTTTTAGGAGATGAAAACAC SEQ ID NO:1253	-8.3	-16.9	53.5	-8.6	0	-3
98	CGGAGACACGGCCCGCGAGG SEQ ID NO:1254	-8.2	-31.3	77	-22	-1	-8.4
823	ACGAGAGAGATTGCAGCTTC SEQ ID NO:1255	-8.2	-23.2	68.5	-15	0	-5.3
826	CACACGAGAGAGATTGCAGC SEQ ID NO:1256	-8.2	-23.4	67.5	-15.2	0	-5.2
837	GTTGTGCTGTCCACACGAGA SEQ ID NO:1257	-8.2	-26.6	75.5	-16.4	-2	-7.2
1100	GCTGCTCAAATATTTCCTTC SEQ ID NO:1258	-8.2	-22.8	67.3	-14.6	0	-6
1288	AGGCAACTCAGTCAGCTCCT SEQ ID NO:1259	-8.2	-27.5	79.5	-18.4	-0.7	-5.7
1446	TTTGTGATCCCCACAGTTAA SEQ ID NO:1260	-8.2	-24.3	69.3	-14	-2.1	-10.8
1886	TCATGATGATCATGATCACA SEQ ID NO:1261	-8.2	-20	61	-8.4	-3.3	-14.2
2484	ACCAATTTTTAGAAACATAT SEQ ID NO:1262	-8.2	-16.1	51.5	-7.9	0	-2.6
2764	AATTTCTTCCACCTACAGAT SEQ ID NO:1263	-8.2	-22.3	65.4	-14.1	0	-2.4
2859	AAAGCAGCTTGAATTTAAAG SEQ ID NO:1264	-8.2	-16.3	51.9	-7.5	0	-8.4
2880	AAATCATATTGTCAGTTGTC SEQ ID NO:1265	-8.2	-18.7	59.5	-10.5	0	-2.1
2943	TTAGGAGATGAAAACACAAA SEQ ID NO:1266	-8.2	-15.1	49.1	-6.9	0	-2.5
134	GGTAGTTTAAGTAAGCAAAT SEQ ID NO:1267	-8.1	-17.8	56.2	-9.7	0	-4.1
145	TCGAGGAACATGGTAGTTTA SEQ ID NO:1268	-8.1	-21	63.1	-12.9	0	-5.2
338	TATCTTGTTGCTTGTGAACT SEQ ID NO:1269	-8.1	-21.4	65.3	-12.8	-0.1	-4.9
469	GTGAATAACGATAAATTCAT SEQ ID NO:1270	-8.1	-15.2	49.3	-5.3	-1.8	-6
628	CTCCACCAAGGTAGTAAAGC SEQ ID NO:1271	-8.1	-23.6	67.7	-15	-0.2	-5.1
944	CATCATCATCTTCCAGAAAG SEQ ID NO:1272	-8.1	-20.6	61.9	-12.5	0	-2.9
1125	CTCATTGTGTTCACGACAGA SEQ ID NO:1273	-8.1	-22.8	67.4	-13.8	-0.7	-6.4
1287	GGCAACTCAGTCAGCTCCTC SEQ ID NO:1274	-8.1	-27.9	81	-19.1	-0.4	-4.9
1724	GAACTGACTTCTGATGATAA SEQ ID NO:1275	-8.1	-18.3	56.8	-10.2	0	-2.7
1727	TCAGAACTGACTTCTGATGA SEQ ID NO:1276	-8.1	-20.4	62.2	-9	-3.3	-9
1733	CCATTATCAGAACTGACTTC SEQ ID NO:1277	-8.1	-20.8	62.5	-12.2	-0.1	-7.6
1885	CATGATGATCATGATCACAG SEQ ID NO:1278	-8.1	-19.6	59.8	-8.4	-2.2	-14.2
2011	CTTGATCGTTCTTTTTGTGT SEQ ID NO:1279	-8.1	-22.2	67.7	-14.1	0	-5.3
2265	TAAGGATTTACTAAAAAAAG SEQ ID NO:1280	-8.1	-11.3	42.1	-3.2	0	-2.9
2266	ATAAGGATTTACTAAAAAAA SEQ ID NO:1281	-8.1	-11.3	42	-3.2	0	-3.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2267	AATAAGGATTTACTAAAAAA SEQ ID NO:1282	-8.1	-11.3	42	-3.2	0	-3.3
2295	TGAGTGGAATAATTATAACT SEQ ID NO:1283	-8.1	-15.8	51.4	-7.7	0	-6.2
139	AACATGGTAGTTTAAGTAAG SEQ ID NO:1284	-8	-16.9	54.6	-8.9	0	-5.2
306	GCCTTAACTTTTCCTTTCTT SEQ ID NO:1285	-8	-24.1	70.5	-16.1	0	-2.2
339	ATATCTTGTTGCTTGTGAAC SEQ ID NO:1286	-8	-20.5	63.3	-12.5	0	-4.1
710	GCCTTGTGCCAACTGCTTGC SEQ ID NO:1287	-8	-29.5	80.6	-20.5	-0.9	-5.8
967	ACGTCCATCCACTACTGCTG SEQ ID NO:1288	-8	-27	74.7	-19	0	-4.4
1085	CCTTCTGCATAAATGAACTG SEQ ID NO:1289	-8	-20.1	59.4	-12.1	0	-4.7
1163	CCAAATTCACAGTATAGTCA SEQ ID NO:1290	-8	-20.3	61.4	-12.3	0	-3.1
1412	TACAGTAACGAAGACCCATC SEQ ID NO:1291	-8	-21.6	62.1	-13.6	0	-3.5
1488	ACTCCACAATCTGTCTCCCG SEQ ID NO:1292	-8	-27.4	75	-19.4	0	-2.4
1575	ATAAGGGCAAACATCACAAG SEQ ID NO:1293	-8	-18.7	56.4	-10.7	0	-4
1605	TCTTGCATGGAGATCCGATC SEQ ID NO:1294	-8	-24.5	70.4	-16	-0.2	-6.3
1618	CTCTTTGCGTCTTTCTTGCA SEQ ID NO:1295	-8	-25.6	75.1	-16.9	-0.4	-4.8
1650	AAATCAGGCAGCCGTTTCAA SEQ ID NO:1296	-8	-23.8	66.9	-15	-0.3	-9
1915	ATTCTGACACTTGGCATAAG SEQ ID NO:1297	-8	-20.8	62.6	-12.3	-0.2	-4.1
2124	AGATTCCGTGGGAAATCAAC SEQ ID NO:1298	-8	-21.3	61.7	-11.4	-1.9	-7.1
2278	ACTGATATATAAATAAGGAT SEQ ID NO:1299	-8	-14.2	48	-6.2	0	-4.2
2296	TTGAGTGGAATAATTATAAC SEQ ID NO:1300	-8	-15	49.9	-7	0	-6.2
2402	AATAGCTAGAATCTTTCTGA SEQ ID NO:1301	-8	-18.7	58.8	-9.8	-0.7	-6.8
2485	TACCAATTTTTAGAAACATA SEQ ID NO:1302	-8	-15.8	50.9	-7.8	0	-2.9
2510	TCTGAATGAAGTATGGTGAA SEQ ID NO:1303	-8	-18.3	56.9	-10.3	0	-2.2
2574	AAGTATGAGCATACACTGCC SEQ ID NO:1304	-8	-22.8	66.7	-13.1	-1.7	-9.6
2884	TTTAAAATCATATTGTCAGT SEQ ID NO:1305	-8	-16.2	52.9	-8.2	0	-4
2961	AGGAAATAAAAAACACTTTT SEQ ID NO:1306	-8	-12.9	44.9	-4.2	-0.4	-2.9
3046	ATAGCAGCTCTGTGTTGTGA SEQ ID NO:1307	-8	-24.5	74.2	-16.5	0	-6.1
132	TAGTTTAAGTAAGCAAATAT SEQ ID NO:1308	-7.9	-15.1	50.3	-7.2	0	-4.1
212	AATCATATCCTCTGTACTCC SEQ ID NO:1309	-7.9	-23.1	68.5	-15.2	0	-4.8
299	CTTTTCCTTTCTTCTTAATA SEQ ID NO:1310	-7.9	-20.2	62.7	-12.3	0	-2.3
518	TGCTTTCCAAAAACTTTTTC SEQ ID NO:1311	-7.9	-19.1	58	-11.2	0	-4.9

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
942	TCATCATCTTCCAGAAAGAT SEQ ID NO:1312	-7.9	-20.5	62	-11	-1.5	-4.7
1026	GTTTGCACAGCTCGTCCGGG SEQ ID NO:1313	-7.9	-29.5	80.5	-21	-0.3	-6.9
1035	ATCTGGAGTGTTTGCACAGC SEQ ID NO:1315	-7.9	-24.9	74.3	-14.3	-2.7	-7.3
1098	TGCTCAAATATTTCCTTCTG SEQ ID NO:1315	-7.9	-21	63	-13.1	0	-5.8
1229	TTCCACAAGCAATAAGAATC SEQ ID NO:1316	-7.9	-18.5	56.3	-10.6	0	-4.1
1233	CTTGTTCCACAAGCAATAAG SEQ ID NO:1317	-7.9	-20.4	60.6	-10.5	-2	-6.5
1518	ACACCAATCTCAGGACCAGC SEQ ID NO:1318	-7.9	-26	72.8	-18.1	0	-3.7
1520	CCACACCAATCTCAGGACCA SEQ ID NO:1319	-7.9	-26.9	72.9	-19	0	-3.7
1892	GATCTCTCATGATGATCATG SEQ ID NO:1320	-7.9	-20.6	63.4	-10.3	-2.4	-11.1
1967	TATCACAAATTACCACAGGC SEQ ID NO:1321	-7.9	-20.9	61.4	-13	0	-3.7
2137	CACAGATTTGGCAAGATTCC SEQ ID NO:1322	-7.9	-22.5	65.7	-14.6	0	-4
2277	CTGATATATAAATAAGGATT SEQ ID NO:1323	-7.9	-14.1	47.8	-6.2	0	-4.2
2585	CCTAACTGTCCAAGTATGAG SEQ ID NO:1324	-7.9	-22.1	64.8	-13.5	-0.5	-3.8
2707	CTTAGATATAAATCCTACCA SEQ ID NO:1325	-7.9	-19.2	58	-10.4	-0.7	-4.2
3059	CAATATTAATTTAATAGCAG SEQ ID NO:1326	-7.9	-14.2	48	-5.6	-0.4	-7.1
28	GGCAATCTGCGGGCTCGGGG SEQ ID NO:1327	-7.8	-30.8	81.1	-20.8	-2.2	-8.4
109	ACACATGATGCCGGAGACAC SEQ ID NO:1328	-7.8	-24.5	68.1	-16.7	0	-6.7
211	ATCATATCCTCTGTACTCCA SEQ ID NO:1329	-7.8	-24.5	72.1	-16.7	0	-4.8
592	CCGATTGTCATACATATACT SEQ ID NO:1330	-7.8	-20.9	61.8	-13.1	0	-4.4
615	GTAAAGCTGGTATCTTGACT SEQ ID NO:1331	-7.8	-21.4	64.9	-13.6	0	-5.3
644	ATTGTTGGATAACTCTCTCC SEQ ID NO:1332	-7.8	-22.3	67.2	-13.4	-1	-4.2
708	CTTGTGCCAACTGCTTGCCC SEQ ID NO:1333	-7.8	-29.7	79.7	-21.4	-0.2	-4.6
1216	AAGAATCAAACGCCGGCATC SEQ ID NO:1334	-7.8	-22.6	62.2	-13.1	0	-11.6
1607	TTTCTTGCATGGAGATCCGA SEQ ID NO:1335	-7.8	-24.3	69.6	-16	-0.2	-6.1
1630	TCCAAGCATGATCTCTTTGC SEQ ID NO:1336	-7.8	-24.1	70.5	-16.3	0.2	-5.1
1801	GTGCATATAAGTAATTTCTT SEQ ID NO:1337	-7.8	-18.2	57.7	-9.9	-0.2	-6.1
1830	TTCAATTCACCAGCAAGGAT SEQ ID NO:1338	-7.8	-22.2	64.6	-13.6	-0.6	-4.9
2071	CAGCAACTGTAAAGGGATCA SEQ ID NO:1339	-7.8	-21.2	62.5	-12	-1.3	-6.6
2076	AAAGCCAGCAACTGTAAAGG SEQ ID NO:1340	-7.8	-20.7	60.1	-11.5	-1.3	-6.9
2225	AAATCAAGGTTTTAAATACA SEQ ID NO:1341	-7.8	-14.6	48.6	-6.8	0	-5.4

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2226	TAAATCAAGGTTTTAAATAC SEQ ID NO:1342	-7.8	-13.6	46.8	-5.8	0	-4.5
2482	CAATTTTTAGAAACATATTG SEQ ID NO:1343	-7.8	-14	47.6	-6.2	0	-2.9
2619	ATCACATCTTCTCTTAAAAC SEQ ID NO:1344	-7.8	-17.9	56.6	-10.1	0	-2.3
2763	ATTTCTTCCACCTACAGATA SEQ ID NO:1345	-7.8	-22.7	67	-14.9	0	-2.4
2780	AATATTTCGCTTCCTAAATT SEQ ID NO:1346	-7.8	-18.9	57.1	-11.1	0	-3.8
300	ACTTTTCCTTTCTTCTTAAT SEQ ID NO:1347	-7.7	-20.7	63.9	-13	0	-2.3
503	TTTTCAAGTCTTTGTAGTTG SEQ ID NO:1348	-7.7	-19.6	62.8	-11.2	-0.5	-3.3
835	TGTGCTGTCCACACGAGAGA SEQ ID NO:1349	-7.7	-25.9	73.4	-16.4	-1.8	-7.2
1019	CAGCTCGTCCGGGGTGATCT SEQ ID NO:1350	-7.7	-29.7	81.3	-22	0	-6.6
1228	TCCACAAGCAATAAGAATCA SEQ ID NO:1351	-7.7	-19.1	57.2	-11.4	0	-4.1
1413	TTACAGTAACGAAGACCCAT SEQ ID NO:1352	-7.7	-21.3	61.1	-13.6	0	-4.5
1509	TCAGGACCAGCATTAATATG SEQ ID NO:1353	-7.7	-21.1	62.6	-13.4	0	-4.2
1516	ACCAATCTCAGGACCAGCAT SEQ ID NO:1354	-7.7	-25.8	72.2	-18.1	0	-4.1
1757	AAGTAGCATAATGATAGCCT SEQ ID NO:1355	-7.7	-20.7	62	-13	0.4	-3.9
1970	CCTTATCACAAATTACCACA SEQ ID NO:1356	-7.7	-20.9	60.7	-13.2	0	-3.2
2305	AATCACATATTGAGTGGAAT SEQ ID NO:1357	-7.7	-18	56.2	-9.4	-0.7	-4.7
2548	TTTAGATACTCCAATTAAAT SEQ ID NO:1358	-7.7	-16.1	51.9	-8.4	0	-3
2583	TAACTGTCCAAGTATGAGCA SEQ ID NO:1359	-7.7	-21.7	64.4	-13.3	-0.5	-5
2799	CCCACCAATGCACTACTGTA SEQ ID NO:1360	-7.7	-26.2	71.4	-18.5	0	-5.5
2838	TTGTGCTATAAAATTGTGCA SEQ ID NO:1361	-7.7	-19.1	58.4	-10.6	-0.6	-5.2
2919	TAGGATACCCAACATGTACA SEQ ID NO:1362	-7.7	-22.1	63.8	-13.3	-1	-8.1
2970	ACAGATACAAGGAAATAAAA SEQ ID NO:1363	-7.7	-13.4	45.7	-5.7	0	-1.3
3053	TAATTTAATAGCAGCTCTGT SEQ ID NO:1364	-7.7	-19.6	60.7	-11.9	0	-6.1
124	GTAAGCAAATATACCACACA SEQ ID NO:1365	-7.6	-19.4	57.9	-11.8	0	-4.1
172	TAGGGTCTCCAGGATTTCTC SEQ ID NO:1366	-7.6	-25.4	76.5	-16.6	-1.1	-5.4
519	TTGCTTTCCAAAAACTTTTT SEQ ID NO:1367	-7.6	-18.8	57.1	-11.2	0	-4.7
642	TGTTGGATAACTCTCTCCAC SEQ ID NO:1368	-7.6	-23.1	68.6	-14.2	-1.2	-5.3
671	TAAACACAAGTGCAAAAGCA SEQ ID NO:1369	-7.6	-17.5	53.5	-9.3	-0.3	-5.8
672	TTAAACACAAGTGCAAAAGC SEQ ID NO:1370	-7.6	-16.9	52.6	-9.3	0	-5.4
1000	TCCTGCAGTTCGTTTAATTC SEQ ID NO:1371	-7.6	-23.2	68.8	-15.1	0	-8.2

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1515	CCAATCTCAGGACCAGCATT SEQ ID NO:1372	-7.6	-25.7	72	-18.1	0	-4.1
2268	AAATAAGGATTTACTAAAAA SEQ ID NO:1373	-7.6	-11.3	42	-3.2	-0.2	-4
2318	GTAACTTCACAAAAATCACA SEQ ID NO:1374	-7.6	-16.6	52.4	-9	0	-1.9
2406	AAATAATAGCTAGAATCTTT SEQ ID NO:1375	-7.6	-15.1	50.1	-7.5	0	-6.3
2680	TTTTCAGTTTTAAGTTTTAC SEQ ID NO:1376	-7.6	-17.3	57	-9.7	0	-2.6
3	GGTGGCGCCGACACGACTCC SEQ ID NO:1377	-7.5	-31.4	79.9	-21.8	-1.6	-12.1
115	TATACCACACATGATGCCGG SEQ ID NO:1378	-7.5	-24.5	67.2	-17	0	-6.4
588	TTGTCATACATATACTTAAC SEQ ID NO:1379	-7.5	-16.8	54.4	-9.3	0	-2.9
643	TTGTTGGATAACTCTCTCCA SEQ ID NO:1380	-7.5	-23	68.4	-14.4	-1	-5.3
1084	CTTCTGCATAAATGAACTGA SEQ ID NO:1381	-7.5	-18.7	57	-11.2	0	-4.9
1293	ATCACAGGCAACTCAGTCAG SEQ ID NO:1382	-7.5	-23.5	69.9	-15.2	-0.6	-4
1420	TCTCTCCTTACAGTAACGAA SEQ ID NO:1383	-7.5	-21.7	64	-14.2	0	-4.7
1487	CTCCACAATCTGTCTCCCGT SEQ ID NO:1384	-7.5	-28.4	77.7	-20.9	0	-2.6
1501	AGCATTAATATGAACTCCAC SEQ ID NO:1385	-7.5	-19.6	59.1	-11.4	-0.4	-4.2
1502	CAGCATTAATATGAACTCCA SEQ ID NO:1386	-7.5	-20.1	59.8	-11.9	-0.4	-4.2
1600	CATGGAGATCCGATCATCAC SEQ ID NO:1387	-7.5	-23.3	66.9	-14.9	-0.7	-7.5
1648	ATCAGGCAGCCGTTTCAATC SEQ ID NO:1388	-7.5	-25.6	72.9	-17.3	-0.3	-9
1813	GATGCCTTCAGAGTGCATAT SEQ ID NO:1389	-7.5	-24.5	71.7	-14.2	-2.8	-6.9
1916	CATTCTGACACTTGGCATAA SEQ ID NO:1390	-7.5	-21.5	63.6	-14	0	-4
2136	ACAGATTTGGCAAGATTCCG SEQ ID NO:1391	-7.5	-22.6	64.8	-14.6	-0.1	-4
2269	TAAATAAGGATTTACTAAAA SEQ ID NO:1392	-7.5	-11.7	42.9	-3.2	-0.8	-5.2
2340	AATTACTGGGAAAATGTAAG SEQ ID NO:1393	-7.5	-15.3	49.8	-7.2	-0.3	-4.1
2444	GAGGGTCCAGAAATGCAACA SEQ ID NO:1394	-7.5	-23.2	66	-14.6	-1	-5.6
2765	AAATTTCTTCCACCTACAGA SEQ ID NO:1395	-7.5	-21.6	63.3	-14.1	0	-4.3
506	ACTTTTTCAAGTCTTTGTAG SEQ ID NO:1396	-7.4	-19.5	62.2	-11.2	-0.8	-3.8
574	CTTAACGAGCTTGGCAATTG SEQ ID NO:1397	-7.4	-21.5	62.3	-13.2	-0.7	-6.3
614	TAAAGCTGGTATCTTGACTT SEQ ID NO:1398	-7.4	-20.3	62	-12.9	0	-5.3
709	CCTTGTGCCAACTGCTTGCC SEQ ID NO:1399	-7.4	-29.7	79.7	-21.3	-0.9	-4.6
945	ACATCATCATCTTCCAGAAA SEQ ID NO:1400	-7.4	-20.8	62.2	-13.4	0	-2.9
1394	TCAAAGTATCTGCTGTCTCA SEQ ID NO:1401	-7.4	-22.2	67.7	-14.8	0	-3.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2337	TACTGGGAAAATGTAAGAGG SEQ ID NO:1402	-7.4	-17.7	54.9	-10.3	0	-2.7
2351	AGTCCTCCACAAATTACTGG SEQ ID NO:1403	-7.4	-23.2	66.8	-15.8	0	-5.3
2365	ATTCCATTATTCAAAGTCCT SEQ ID NO:1404	-7.4	-21.3	63.5	-13.9	0	-1.6
2662	ACAGTTTGATTTAAAAACAA SEQ ID NO:1405	-7.4	-14.2	47.7	-5.1	-1.7	-6.9
2677	TCAGTTTTAAGTTTTACAGT SEQ ID NO:1406	-7.4	-18.9	60.8	-11.5	0	-2.6
2697	AATCCTACCAATAAAATTTT SEQ ID NO:1407	-7.4	-16.4	51.4	-9	0	-6.5
2708	ACTTAGATATAAATCCTACC SEQ ID NO:1408	-7.4	-18.7	57.3	-10.4	-0.7	-3.4
2781	TAATATTTCGCTTCCTAAAT SEQ ID NO:1409	-7.4	-18.5	56.3	-11.1	0	-4.2
2947	ACTTTTAGGAGATGAAAACA SEQ ID NO:1410	-7.4	-16.9	53.5	-9.5	0	-3
2967	GATACAAGGAAATAAAAAAC SEQ ID NO:1411	-7.4	-11.3	41.8	-3.9	0	-1.3
3000	ATTCAGCAGTCATTTAAAAA SEQ ID NO:1412	-7.4	-17.1	54.3	-9.7	0	-5
110	CACACATGATGCCGGAGACA SEQ ID NO:1413	-7.3	-25	68.6	-17.7	0	-6.7
237	CCTCCATCAAATCCCACACC SEQ ID NO:1415	-7.3	-27.9	73.4	-20.6	0	-1.1
460	GATAAATTCATTATTTTTAT SEQ ID NO:1415	-7.3	-14	48.1	-6	-0.5	-5.9
468	TGAATAACGATAAATTCATT SEQ ID NO:1416	-7.3	-14.1	47.2	-5.3	-1.4	-5.3
645	AATTGTTGGATAACTCTCTC SEQ ID NO:1417	-7.3	-19.6	61.1	-11.2	-1	-4.4
769	AATGTGATCAGTAGAAAGTT SEQ ID NO:1418	-7.3	-17.6	56.1	-10.3	0	-6.6
810	CAGCTTCCTTTCTTGTCTTT SEQ ID NO:1419	-7.3	-25.1	75.4	-17.8	0	-4.5
815	GATTGCAGCTTCCTTTCTTG SEQ ID NO:1420	-7.3	-24.9	73.3	-17.6	0	-5.2
873	TACTCCACTGCTTTTTCTTC SEQ ID NO:1421	-7.3	-23.9	71.7	-16.6	0	-3.6
1037	CCATCTGGAGTGTTTGCACA SEQ ID NO:1422	-7.3	-25.8	74.4	-15.8	-2.7	-8.8
1099	CTGCTCAAATATTTCCTTCT SEQ ID NO:1423	-7.3	-21.9	65.1	-14.6	0	-6
1694	CTAGTTTCTGAATTTCGTCA SEQ ID NO:1424	-7.3	-20.9	64	-13.6	0	-5
1715	TCTGATGATAAAGTTCTGTT SEQ ID NO:1425	-7.3	-18.7	59	-11.4	0	-2.5
1732	CATTATCAGAACTGACTTCT SEQ ID NO:1426	-7.3	-19.7	60.7	-11.6	-0.6	-7.1
1825	TTCACCAGCAAGGATGCCTT SEQ ID NO:1427	-7.3	-26.5	73.7	-17	-2.2	-5.9
2133	GATTTGGCAAGATTCCGTGG SEQ ID NO:1428	-7.3	-24.1	68.3	-16.8	0.6	-4
2279	AACTGATATATAAATAAGGA SEQ ID NO:1429	-7.3	-13.5	46.4	-6.2	0	-4
2366	GATTCCATTATTCAAAGTCC SEQ ID NO:1430	-7.3	-21	62.9	-13.7	0	-1.9
2443	AGGGTCCAGAAATGCAACAC SEQ ID NO:1431	-7.3	-22.8	65.3	-14.4	-1	-5.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2816	TATGTTAAGGATTGAGACCC SEQ ID NO:1432	-7.3	-21.3	63.1	-14	0	-3.2
3002	TCATTCAGCAGTCATTTAAA SEQ ID NO:1433	-7.3	-19.6	60.8	-12.3	0	-4.6
40	CGAGCTTCGGTGGGCAATCT SEQ ID NO:1434	-7.2	-27.3	74.9	-19.2	-0.8	-5.8
200	TGTACTCCAGTCTCTGAAGG SEQ ID NO:1435	-7.2	-24	71.7	-16.2	-0.3	-5.2
623	CCAAGGTAGTAAAGCTGGTA SEQ ID NO:1436	-7.2	-22.4	65.8	-15.2	0	-5.1
707	TTGTGCCAACTGCTTGCCCG SEQ ID NO:1437	-7.2	-29.6	77.6	-21.4	-0.9	-4.4
872	ACTCCACTGCTTTTTCTTCC SEQ ID NO:1438	-7.2	-26.2	76.1	-19	0	-3.6
1097	GCTCAAATATTTCCTTCTGC SEQ ID NO:1439	-7.2	-22.8	67.3	-15.6	0	-6
1170	AAACCACCCAAATTCACAGT SEQ ID NO:1440	-7.2	-22.3	62.3	-15.1	0	-3.1
1263	ACTTGACGTGTTGCTACACC SEQ ID NO:1441	-7.2	-24.8	70.7	-15.5	-2.1	-5.6
1280	CAGTCAGCTCCTCAAGAACT SEQ ID NO:1442	-7.2	-24.4	71.1	-17.2	0	-4.2
1508	CAGGACCAGCATTAATATGA SEQ ID NO:1443	-7.2	-21.3	62.5	-13.4	-0.4	-4.2
1632	AATCCAAGCATGATCTCTTT SEQ ID NO:1444	-7.2	-21.6	64.1	-14.4	0	-4.9
1719	GACTTCTGATGATAAAGTTC SEQ ID NO:1445	-7.2	-18.3	57.9	-10.2	-0.7	-4
1754	TAGCATAATGATAGCCTCGT SEQ ID NO:1446	-7.2	-22.6	65.6	-14.9	-0.1	-4.1
1820	CAGCAAGGATGCCTTCAGAG SEQ ID NO:1447	-7.2	-24.8	71	-15.4	-2.2	-6.7
1901	CATAAGTGTGATCTCTCATG SEQ ID NO:1448	-7.2	-20.4	63.1	-12.5	-0.4	-4.9
2013	ACCTTGATCGTTCTTTTTGT SEQ ID NO:1449	-7.2	-23.2	68.9	-16	0	-4.6
2087	CAGCAAGGTGGAAAGCCAGC SEQ ID NO:1450	-7.2	-25.6	71.3	-18.4	3.5	-6.5
2130	TTGGCAAGATTCCGTGGGAA SEQ ID NO:1451	-7.2	-24.5	68.3	-16	-1.2	-6.4
2135	CAGATTTGGCAAGATTCCGT SEQ ID NO:1452	-7.2	-23.6	67.3	-15.9	-0.1	-4
2224	AATCAAGGTTTTAAATACAA SEQ ID NO:1453	-7.2	-14.6	48.6	-7.4	0	-5.4
2339	ATTACTGGGAAAATGTAAGA SEQ ID NO:1454	-7.2	-16.6	52.7	-8.8	-0.3	-4.1
2533	TAAATGCACTACTCTTTCAC SEQ ID NO:1455	-7.2	-19.5	59.9	-12.3	0	-5.5
2881	AAAATCATATTGTCAGTTGT SEQ ID NO:1456	-7.2	-17.6	56.1	-10.4	0	-2.1
2953	AAAAACACTTTTAGGAGATG SEQ ID NO:1457	-7.2	-15.6	50.6	-7.8	-0.3	-3
3054	TTAATTTAATAGCAGCTCTG SEQ ID NO:1458	-7.2	-18.5	57.9	-11.3	0	-6.1
104	TGATGCCGGAGACACGGCCC SEQ ID NO:1459	-7.1	-30.5	77.7	-19.3	-4.1	-10.6
450	TTATTTTTATCAGAGCGCTG SEQ ID NO:1460	-7.1	-20.9	63.2	-12.8	-0.8	-9.4
617	TAGTAAAGCTGGTATCTTGA SEQ ID NO:1461	-7.1	-20	61.9	-12.9	0	-5.1

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
958	CACTACTGCTGCAACATCAT SEQ ID NO:1462	-7.1	-23.1	66.8	-16	0	-7.3
1395	ATCAAAGTATCTGCTGTCTC SEQ ID NO:1463	-7.1	-21.5	66.4	-14.4	0	-3.6
1601	GCATGGAGATCCGATCATCA SEQ ID NO:1464	-7.1	-24.9	70.5	-16.9	-0.7	-7.5
1700	CTGTTGCTAGTTTCTGAATT SEQ ID NO:1465	-7.1	-21.3	65.5	-14.2	0	-4.7
1709	GATAAAGTTCTGTTGCTAGT SEQ ID NO:1466	-7.1	-20.4	63.5	-13.3	0	-4.1
1955	CCACAGGCCGCCCCTGCCGA SEQ ID NO:1467	-7.1	-37.3	88.1	-27.4	-2.8	-9
2139	GTCACAGATTTGGCAAGATT SEQ ID NO:1468	-7.1	-21.7	65.1	-14.6	0	-4.1
2270	ATAAATAAGGATTTACTAAA SEQ ID NO:1469	-7.1	-12.4	44.3	-3.9	-1.3	-5
2304	ATCACATATTGAGTGGAATA SEQ ID NO:1470	-7.1	-18.4	57.5	-10.4	-0.7	-5
2456	CAGATTGAAGTGGAGGGTCC SEQ ID NO:1471	-7.1	-24.3	71	-16.5	-0.4	-3.5
2847	ATTTAAAGTTTGTGCTATAA SEQ ID NO:1472	-7.1	-16.5	53.5	-9.4	0	-4.9
3003	GTCATTCAGCAGTCATTTAA SEQ ID NO:1473	-7.1	-21.5	66.3	-14.4	0	-4.1
73	GGCGAGTGGCTGGCGGGATC SEQ ID NO:1474	-7	-30.7	82.7	-22	-1.7	-6.5
144	CGAGGAACATGGTAGTTTAA SEQ ID NO:1475	-7	-19.9	59.7	-12.9	0	-5.2
150	CTCGTTCGAGGAACATGGTA SEQ ID NO:1476	-7	-23.3	66.8	-14.4	-1.9	-8.1
257	CTTCCCAATCTTTATCATTG SEQ ID NO:1477	-7	-21.8	64.4	-14.8	0	-3.3
711	CGCCTTGTGCCAACTGCTTG SEQ ID NO:1478	-7	-28.5	76.1	-20.5	-0.9	-6.1
836	TTGTGCTGTCCACACGAGAG SEQ ID NO:1479	-7	-25.4	72.4	-16.4	-2	-7.2
1188	TCCTTTATGTGATCCTTCAA SEQ ID NO:1480	-7	-22.8	67.3	-15.1	-0.5	-5.5
1206	CGCCGGCATCTCTGGATCTC SEQ ID NO:1481	-7	-29.2	79.4	-20.6	-0.9	-11.3
1860	AATTTATCCACCAAAGCCAG SEQ ID NO:1482	-7	-22.3	63	-15.3	0	-3.2
2367	AGATTCCATTATTCAAAGTC SEQ ID NO:1483	-7	-19	59.3	-12	0	-2.6
2506	AATGAAGTATGGTGAAACAA SEQ ID NO:1484	-7	-15.9	50.9	-7.9	-0.9	-3.9
2535	ATTAAATGCACTACTCTTTC SEQ ID NO:1485	-7	-18.7	58.4	-11.7	0	-5.5
2778	TATTTCGCTTCCTAAATTTC SEQ ID NO:1486	-7	-20.1	60.7	-13.1	0	-4.9
2815	ATGTTAAGGATTGAGACCCA SEQ ID NO:1487	-7	-22.3	64.9	-14.8	-0.2	-3.4
2917	GGATACCCAACATGTACACA SEQ ID NO:1488	-7	-23.3	65.8	-15.8	-0.2	-7.1
2971	TACAGATACAAGGAAATAAA SEQ ID NO:1489	-7	-13.8	46.7	-6.8	0	-1.2
201	CTGTACTCCAGTCTCTGAAG SEQ ID NO:1490	-6.9	-23.7	71	-16.2	-0.3	-5.2
572	TAACGAGCTTGGCAATTGTC SEQ ID NO:1491	-6.9	-22.1	64.4	-14.3	-0.7	-7.5

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
616	AGTAAAGCTGGTATCTTGAC SEQ ID NO:1492	-6.9	-20.5	63.1	-13.6	0	-4.6
1327	GTTTCTGTCCAGGAAGTCAC SEQ ID NO:1493	-6.9	-24.6	73.9	-17.2	-0.1	-5.5
1334	CTGGTGTGTTTCTGTCCAGG SEQ ID NO:1494	-6.9	-26.7	79.3	-18.3	-1.4	-5.5
1445	TTGTGATCCCCACAGTTAAA SEQ ID NO:1495	-6.9	-23.5	66.8	-14.5	-2.1	-10.8
1458	CTGCCAACTGTGTTTGTGAT SEQ ID NO:1496	-6.9	-24.2	70.1	-17.3	0	-3.3
1604	CTTGCATGGAGATCCGATCA SEQ ID NO:1497	-6.9	-24.8	69.9	-17	-0.7	-7.5
1690	TTTCTGAATTTCGTCATCCA SEQ ID NO:1498	-6.9	-22.2	65.6	-15.3	0	-4.7
1763	CAAGACAAGTAGCATAATGA SEQ ID NO:1499	-6.9	-17.8	55.3	-10.9	0	-4.1
1802	AGTGCATATAAGTAATTTCT SEQ ID NO:1500	-6.9	-18.1	57.6	-10.7	-0.2	-6.1
2826	ATTGTGCAAATATGTTAAGG SEQ ID NO:1501	-6.9	-17.6	55.3	-10.7	0	-6.1
2906	ATGTACACATCCCATCTTCA SEQ ID NO:1502	-6.9	-24.3	70.4	-17.4	0	-6.7
2907	CATGTACACATCCCATCTTC SEQ ID NO:1503	-6.9	-24.3	70.4	-17.4	0	-6.7
2913	ACCCAACATGTACACATCCC SEQ ID NO:1504	-6.9	-26.2	71	-19.3	0	-6.7
2941	AGGAGATGAAAACACAAAGT SEQ ID NO:1505	-6.9	-16.5	52	-9.6	0	-2.8
44	CACACGAGCTTCGGTGGGCA SEQ ID NO:1506	-6.8	-28.5	77	-19.4	-2.3	-9.5
258	GCTTCCCAATCTTTATCATT SEQ ID NO:1507	-6.8	-23.6	68.7	-16.8	0	-2.8
472	ATTGTGAATAACGATAAATT SEQ ID NO:1508	-6.8	-14.2	47.4	-6.8	-0.3	-3.5
562	GGCAATTGTCTCTGTGTCTG SEQ ID NO:1509	-6.8	-24.6	74	-17.3	0	-7.6
612	AAGCTGGTATCTTGACTTTC SEQ ID NO:1510	-6.8	-21.8	66.8	-15	0	-5.3
883	AGCAAAGTAATACTCCACTG SEQ ID NO:1511	-6.8	-20.3	60.6	-13.5	0	-5.1
1027	TGTTTGCACAGCTCGTCCGG SEQ ID NO:1512	-6.8	-28.3	77.7	-21	-0.1	-6.1
1289	CAGGCAACTCAGTCAGCTCC SEQ ID NO:1513	-6.8	-27.3	78.5	-19.6	-0.8	-5.8
1422	CCTCTCTCCTTACAGTAACG SEQ ID NO:1515	-6.8	-24.7	70.4	-17.9	0	-4.7
1712	GATGATAAAGTTCTGTTGCT SEQ ID NO:1515	-6.8	-20.1	61.8	-13.3	0	-3.6
1753	AGCATAATGATAGCCTCGTC SEQ ID NO:1516	-6.8	-23.3	67.7	-16	-0.1	-4.1
1889	CTCTCATGATGATCATGATC SEQ ID NO:1517	-6.8	-20.6	63.4	-10.3	-3.5	-11.3
1949	GCCGCCCCTGCCGAGCAACC SEQ ID NO:1518	-6.8	-36.5	86.5	-28.6	-1	-7.1
2188	CTTAATCATACAGTTTCGTA SEQ ID NO:1519	-6.8	-19.2	59.5	-12.4	0	-3.1
2509	CTGAATGAAGTATGGTGAAA SEQ ID NO:1520	-6.8	-17.2	53.9	-10.4	0	-1.3
2540	CTCCAATTAAATGCACTACT SEQ ID NO:1521	-6.8	-20.1	59.5	-13.3	0	-5.5

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2549	CTTTAGATACTCCAATTAAA SEQ ID NO:1522	-6.8	-17	53.7	-10.2	0	-3
2593	AACCCTTCCCTAACTGTCCA SEQ ID NO:1523	-6.8	-28.2	75.2	-21.4	0	-3.2
2800	ACCCACCAATGCACTACTGT SEQ ID NO:1524	-6.8	-26.7	72.5	-19.9	0	-5.5
2837	TGTGCTATAAAATTGTGCAA SEQ ID NO:1525	-6.8	-18.3	56.2	-10.6	-0.8	-5.7
2885	ATTTAAAATCATATTGTCAG SEQ ID NO:1526	-6.8	-15	50.1	-8.2	0	-5
2918	AGGATACCCAACATGTACAC SEQ ID NO:1527	-6.8	-22.6	64.9	-14.7	-1	-8.1
68	GTGGCTGGCGGGATCGGGGG SEQ ID NO:1528	-6.7	-31.9	84.3	-24.3	-0.7	-6.3
218	CAGCAGAATCATATCCTCTG SEQ ID NO:1529	-6.7	-22.5	66.5	-14.9	-0.8	-4.4
297	TTTCCTTTCTTCTTAATAAG SEQ ID NO:1530	-6.7	-18.5	58.5	-11.8	0	-4.8
520	TTTGCTTTCCAAAAACTTTT SEQ ID NO:1531	-6.7	-18.8	57.1	-11.2	-0.8	-4.1
593	CCCGATTGTCATACATATAC SEQ ID NO:1532	-6.7	-22	63.6	-15.3	0	-4.4
670	AAACACAAGTGCAAAAGCAC SEQ ID NO:1533	-6.7	-18	54.4	-9.3	-2	-8.6
1083	TTCTGCATAAATGAACTGAA SEQ ID NO:1534	-6.7	-17.1	53.5	-10.4	0	-4.9
1174	CTTCAAACCACCCAAATTCA SEQ ID NO:1535	-6.7	-22.3	62.2	-15.6	0	-3.1
1281	TCAGTCAGCTCCTCAAGAAC SEQ ID NO:1536	-6.7	-23.9	70.7	-17.2	0	-4.4
1407	TAACGAAGACCCATCAAAGT SEQ ID NO:1537	-6.7	-20.3	58.5	-12.9	-0.4	-3.9
1408	GTAACGAAGACCCATCAAAG SEQ ID NO:1538	-6.7	-20.3	58.5	-12.9	-0.4	-3.9
1491	TGAACTCCACAATCTGTCTC SEQ ID NO:1539	-6.7	-22.5	66.7	-15.8	0	-2.6
1636	TTTCAATCCAAGCATGATCT SEQ ID NO:1540	-6.7	-21.4	63.4	-14.7	0	-4.9
1734	CCCATTATCAGAACTGACTT SEQ ID NO:1541	-6.7	-22.4	64.8	-15.2	-0.1	-7.6
1812	ATGCCTTCAGAGTGCATATA SEQ ID NO:1542	-6.7	-23.6	69.7	-14.7	-2.2	-6.2
1961	AAATTACCACAGGCCGCCCC SEQ ID NO:1543	-6.7	-29.8	75.1	-22.6	-0.2	-7.7
2364	TTCCATTATTCAAAGTCCTC SEQ ID NO:1544	-6.7	-21.7	65	-15	0	-1.6
2584	CTAACTGTCCAAGTATGAGC SEQ ID NO:1545	-6.7	-21.9	65.2	-14.5	-0.5	-3.7
2595	CAAACCCTTCCCTAACTGTC SEQ ID NO:1546	-6.7	-25.5	69.7	-18.8	0	-3.2
2608	TCTTAAAACTTGGCAAACCC SEQ ID NO:1547	-6.7	-20.7	59.6	-13.3	-0.5	-4
2999	TTCAGCAGTCATTTAAAAAA SEQ ID NO:1548	-6.7	-16.4	52.5	-9.7	0	-5
3057	ATATTAATTTAATAGCAGCT SEQ ID NO:1549	-6.7	-16.9	54.2	-9.5	-0.4	-7.1
3058	AATATTAATTTAATAGCAGC SEQ ID NO:1550	-6.7	-15.3	50.5	-7.9	-0.4	-7.1
107	ACATGATGCCGGAGACACGG SEQ ID NO:1551	-6.6	-25.6	69	-17.4	-1.5	-8.2

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
142	AGGAACATGGTAGTTTAAGT SEQ ID NO:1552	-6.6	-19.7	61.1	-13.1	0	-4.3
252	CAATCTTTATCATTGCCTCC SEQ ID NO:1553	-6.6	-23.5	68.2	-16.9	0	-3
466	AATAACGATAAATTCATTAT SEQ ID NO:1554	-6.6	-13.2	45.5	-6	-0.3	-3.1
800	TCTTGTCTTTGCCTGTTCTG SEQ ID NO:1555	-6.6	-25.4	76.3	-18.8	0	-3
957	ACTACTGCTGCAACATCATC SEQ ID NO:1556	-6.6	-22.8	67.2	-16.2	0	-7.1
1021	CACAGCTCGTCCGGGGTGAT SEQ ID NO:1557	-6.6	-29.3	79.2	-21.7	-0.9	-7.1
1022	GCACAGCTCGTCCGGGGTGA SEQ ID NO:1558	-6.6	-31.1	83.6	-23.5	-0.9	-7.5
1154	CAGTATAGTCATCAAAGTTG SEQ ID NO:1559	-6.6	-18.6	58.9	-12	0	-3.3
1397	CCATCAAAGTATCTGCTGTC SEQ ID NO:1560	-6.6	-22.9	67.9	-16.3	0	-3.6
1728	ATCAGAACTGACTTCTGATG SEQ ID NO:1561	-6.6	-19.8	60.8	-9	-4.2	-9.9
1811	TGCCTTCAGAGTGCATATAA SEQ ID NO:1562	-6.6	-22.9	67.4	-14.8	-1.4	-5.6
1834	ATGTTTCAATTCACCAGCAA SEQ ID NO:1563	-6.6	-21.7	63.9	-15.1	0	-4.1
2174	TTCGTACATTTTGTATAGAT SEQ ID NO:1564	-6.6	-18.6	58.5	-11.1	-0.8	-4.8
2789	CACTACTGTAATATTTCGCT SEQ ID NO:1565	-6.6	-20.6	61.8	-14	0	-4.2
2998	TCAGCAGTCATTTAAAAAAT SEQ ID NO:1566	-6.6	-16.3	52.2	-9.7	0	-5
52	GGGGTGCACACACGAGCTTC SEQ ID NO:1567	-6.5	-27.9	77.9	-19	-2.4	-9.8
194	CCAGTCTCTGAAGGCCTTTG SEQ ID NO:1568	-6.5	-26.5	75.4	-18.5	-0.3	-10.9
255	TCCCAATCTTTATCATTGCC SEQ ID NO:1569	-6.5	-24.6	69.9	-17.6	-0.1	-3.4
573	TTAACGAGCTTGGCAATTGT SEQ ID NO:1570	-6.5	-21.8	63.4	-14.4	-0.7	-7
1032	TGGAGTGTTTGCACAGCTCG SEQ ID NO:1571	-6.5	-25.7	74.2	-16.4	-2.8	-9.1
1161	AAATTCACAGTATAGTCATC SEQ ID NO:1572	-6.5	-18	57.6	-11.5	0	-3.1
1608	CTTTCTTGCATGGAGATCCG SEQ ID NO:1573	-6.5	-24.6	70.2	-17.6	-0.2	-6.4
1725	AGAACTGACTTCTGATGATA SEQ ID NO:1574	-6.5	-19	58.9	-11.7	-0.6	-3.2
1835	CATGTTTCAATTCACCAGCA SEQ ID NO:1575	-6.5	-23.1	67.3	-16.6	0	-4.1
1913	TCTGACACTTGGCATAAGTG SEQ ID NO:1576	-6.5	-21.9	65.4	-13.2	-2.2	-8.8
1940	GCCGAGCAACCACTTGCTGA SEQ ID NO:1577	-6.5	-28.4	75.4	-18.3	-3.6	-8.8
1941	TGCCGAGCAACCACTTGCTG SEQ ID NO:1578	-6.5	-27.8	74	-18.3	-3	-9.8
2018	GGGGCACCTTGATCGTTCTT SEQ ID NO:1579	-6.5	-27.8	77.8	-19.3	-2	-10.7
2095	TCTCAGCACAGCAAGGTGGA SEQ ID NO:1580	-6.5	-25.8	74.9	-18.4	-0.7	-5.1
2120	TCCGTGGGAAATCAACATCA SEQ ID NO:1581	-6.5	-22.4	63.5	-15.4	-0.2	-4.8

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2121	TTCCGTGGGAAATCAACATC SEQ ID NO:1582	-6.5	-21.8	62.7	-14.3	-0.9	-5.5
2134	AGATTTGGCAAGATTCCGTG SEQ ID NO:1583	-6.5	-22.9	66.1	-15.9	-0.1	-4
2314	CTTCACAAAAATCACATATT SEQ ID NO:1584	-6.5	-16	51.3	-9.5	0	-2.1
2698	AAATCCTACCAATAAAATTT SEQ ID NO:1585	-6.5	-15.6	49.6	-9.1	0	-4.9
2960	GGAAATAAAAAACACTTTTA SEQ ID NO:1586	-6.5	-12.6	44.3	-5.3	-0.6	-3.7
45	ACACACGAGCTTCGGTGGGC SEQ ID NO:1587	-6.4	-28	76.5	-18.4	-3.2	-10.9
81	AGGCCAGGGGCGAGTGGCTG SEQ ID NO:1588	-6.4	-31.6	85.3	-21.9	-3.3	-9.8
424	GCTATTGACAGGACTGGGTT SEQ ID NO:1589	-6.4	-24.6	72.1	-18.2	0	-5.8
585	TCATACATATACTTAACGAG SEQ ID NO:1590	-6.4	-16.9	53.5	-10.5	0	-3.5
613	AAAGCTGGTATCTTGACTTT SEQ ID NO:1591	-6.4	-20.7	63	-14.3	0	-5.3
653	CACCTTCCAATTGTTGGATA SEQ ID NO:1592	-6.4	-23.2	66.7	-14.4	-2.4	-7.9
889	ATCAGAAGCAAAGTAATACT SEQ ID NO:1593	-6.4	-17.1	54.1	-10.7	0	-5.4
959	CCACTACTGCTGCAACATCA SEQ ID NO:1594	-6.4	-25.1	70.4	-18.7	0	-7.3
1166	CACCCAAATTCACAGTATAG SEQ ID NO:1595	-6.4	-20.9	61.3	-14.5	0	-3.1
1511	TCTCAGGACCAGCATTAATA SEQ ID NO:1596	-6.4	-22.4	66.1	-16	0	-4.2
1635	TTCAATCCAAGCATGATCTC SEQ ID NO:1597	-6.4	-21.7	64.5	-15.3	0	-4.9
1718	ACTTCTGATGATAAAGTTCT SEQ ID NO:1598	-6.4	-18.6	58.5	-11.7	-0.1	-3.6
1911	TGACACTTGGCATAAGTGTG SEQ ID NO:1599	-6.4	-21.8	65	-11	-4.4	-11.2
2019	TGGGGCACCTTGATCGTTCT SEQ ID NO:1600	-6.4	-27.7	77.3	-19.3	-2	-10.7
2103	TCATAGCCTCTCAGCACAGC SEQ ID NO:1601	-6.4	-27.1	78.8	-20.7	0.1	-4.1
2173	TCGTACATTTTGTATAGATA SEQ ID NO:1602	-6.4	-18.2	57.6	-10.9	-0.8	-4.8
2594	AAACCCTTCCCTAACTGTCC SEQ ID NO:1603	-6.4	-26.8	72	-20.4	0	-3.2
2681	TTTTTCAGTTTTAAGTTTTA SEQ ID NO:1604	-6.4	-17.2	56.8	-10.8	0	-2.6
2706	TTAGATATAAATCCTACCAA SEQ ID NO:1605	-6.4	-17.6	54.4	-10.4	-0.6	-4.2
2912	CCCAACATGTACACATCCCA SEQ ID NO:1606	-6.4	-26.7	71.5	-20.3	0	-7
2972	CTACAGATACAAGGAAATAA SEQ ID NO:1607	-6.4	-15.4	50	-9	0	-1.4
341	CCATATCTTGTTGCTTGTGA SEQ ID NO:1608	-6.3	-23.7	70.1	-17.4	0	-3.6
597	CTTTCCCGATTGTCATACAT SEQ ID NO:1609	-6.3	-23.9	68.1	-17.6	0	-4.4
979	ATGGATAGAAAGACGTCCAT SEQ ID NO:1610	-6.3	-20.6	60.4	-12.7	-1.6	-8.6
1020	ACAGCTCGTCCGGGGTGATC SEQ ID NO:1611	-6.3	-29	80	-21.7	-0.9	-7.1

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1118	TGTTCACGACAGACTCTGGC SEQ ID NO:1612	-6.3	-24.9	72.1	-17.7	-0.7	-6.8
1495	AATATGAACTCCACAATCTG SEQ ID NO:1613	-6.3	-18.6	56.5	-12.3	0	-2.7
1810	GCCTTCAGAGTGCATATAAG SEQ ID NO:1615	-6.3	-22.9	67.8	-15.7	-0.7	-5.4
1822	ACCAGCAAGGATGCCTTCAG SEQ ID NO:1615	-6.3	-26.4	73.6	-17.9	-2.2	-5.9
1965	TCACAAATTACCACAGGCCG SEQ ID NO:1616	-6.3	-24	65.8	-17.2	0	-7.7
2221	CAAGGTTTTAAATACAAAAG SEQ ID NO:1617	-6.3	-13.5	46.2	-7.2	0	-5.4
2607	CTTAAAACTTGGCAAACCCT SEQ ID NO:1618	-6.3	-21.2	60.1	-14.2	-0.5	-4
2774	TCGCTTCCTAAATTTCTTCC SEQ ID NO:1619	-6.3	-23.6	67.8	-17.3	0	-4.9
2954	AAAAAACACTTTTAGGAGAT SEQ ID NO:1620	-6.3	-14.9	49	-7.8	-0.6	-3
3004	TGTCATTCAGCAGTCATTTA SEQ ID NO:1621	-6.3	-22.2	68.7	-15.9	0	-4.1
3047	AATAGCAGCTCTGTGTTGTG SEQ ID NO:1622	-6.3	-23.2	70.2	-16.9	0	-6.1
203	CTCTGTACTCCAGTCTCTGA SEQ ID NO:1623	-6.2	-25.7	77.3	-18.6	-0.8	-5.2
343	ATCCATATCTTGTTGCTTGT SEQ ID NO:1624	-6.2	-23.5	70.5	-17.3	0	-3.6
507	AACTTTTTCAAGTCTTTGTA SEQ ID NO:1625	-6.2	-18.8	59.7	-11.2	-1.3	-4.3
675	CTTTTAAACACAAGTGCAAA SEQ ID NO:1626	-6.2	-16.9	52.8	-10.7	0	-5.8
824	CACGAGAGAGATTGCAGCTT SEQ ID NO:1627	-6.2	-23.5	68.1	-17.3	0	-5.3
850	CGGGAAAAGGCAGGTTGTGC SEQ ID NO:1628	-6.2	-24.9	69.4	-17.2	-1.4	-4.8
938	CATCTTCCAGAAAGATGACG SEQ ID NO:1629	-6.2	-20.6	60.3	-11	-3.4	-8.5
999	CCTGCAGTTCGTTTAATTCG SEQ ID NO:1630	-6.2	-23.6	67.4	-16.9	0	-8.2
1623	ATGATCTCTTTGCGTCTTTC SEQ ID NO:1631	-6.2	-23.1	70	-16.9	0	-4.9
1705	AAGTTCTGTTGCTAGTTTCT SEQ ID NO:1632	-6.2	-22.3	69.7	-16.1	0	-4.1
1920	AGAGCATTCTGACACTTGGC SEQ ID NO:1633	-6.2	-24.2	71.4	-18	0	-4.1
1968	TTATCACAAATTACCACAGG SEQ ID NO:1634	-6.2	-19.2	57.9	-13	0	-3.6
2062	TAAAGGGATCACGCTGAGAA SEQ ID NO:1635	-6.2	-20.6	60.2	-13.9	-0.1	-5.3
2271	TATAAATAAGGATTTACTAA SEQ ID NO:1636	-6.2	-12.8	45.2	-5.2	-1.3	-4.1
2478	TTTTAGAAACATATTGTCTT SEQ ID NO:1637	-6.2	-16.5	53.7	-9.8	-0.2	-4
2479	TTTTTAGAAACATATTGTCT SEQ ID NO:1638	-6.2	-16.5	53.7	-9.8	-0.2	-4
2620	AATCACATCTTCTCTTAAAA SEQ ID NO:1639	-6.2	-17	54.3	-10.8	0	-2.3
2784	CTGTAATATTTCGCTTCCTA SEQ ID NO:1640	-6.2	-22	64.9	-15.8	0	-4.2
3042	CAGCTCTGTGTTGTGATTTT SEQ ID NO:1641	-6.2	-23.3	71.1	-17.1	0	-4.4

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
39	GAGCTTCGGTGGGCAATCTG SEQ ID NO:1642	-6.1	-26.5	74.9	-19.5	-0.8	-5.2
516	CTTTCCAAAAACTTTTTCAA SEQ ID NO:1643	-6.1	-17.3	53.7	-11.2	0	-4.9
541	TTCAGATTCGAAGTCATAGC SEQ ID NO:1644	-6.1	-20.8	63.4	-14.2	-0.1	-7.6
638	GGATAACTCTCTCCACCAAG SEQ ID NO:1645	-6.1	-23.8	68.1	-17.1	-0.3	-3.6
676	ACTTTTAAACACAAGTGCAA SEQ ID NO:1646	-6.1	-17.8	55	-11.7	0	-5.8
913	GGTGTGTTCTATGACAGCAC SEQ ID NO:1647	-6.1	-24.1	72.6	-16.4	-1.6	-5.8
925	GATGACGCGATTGGTGTGTT SEQ ID NO:1648	-6.1	-24.4	69.2	-17.4	-0.8	-7
931	CAGAAAGATGACGCGATTGG SEQ ID NO:1649	-6.1	-20.6	59.1	-14	0	-7.9
1294	CATCACAGGCAACTCAGTCA SEQ ID NO:1650	-6.1	-24.2	70.8	-17.2	-0.8	-4
1404	CGAAGACCCATCAAAGTATC SEQ ID NO:1651	-6.1	-21.2	61	-14.4	-0.4	-2.8
1512	ATCTCAGGACCAGCATTAAT SEQ ID NO:1652	-6.1	-22.7	66.6	-16.6	0	-4.1
1543	GCTGGTATAAGCCTTTGTAC SEQ ID NO:1653	-6.1	-23.8	70.2	-16.6	-1	-5.2
1750	ATAATGATAGCCTCGTCCCA SEQ ID NO:1654	-6.1	-25.5	70.5	-19.4	0	-3.2
1893	TGATCTCTCATGATGATCAT SEQ ID NO:1655	-6.1	-20.6	63.4	-11.9	-2.5	-12.4
2015	GCACCTTGATCGTTCTTTTT SEQ ID NO:1656	-6.1	-24.5	71.2	-18.4	0	-5.3
2368	TAGATTCCATTATTCAAAGT SEQ ID NO:1657	-6.1	-18.3	57.3	-12.2	0	-2.6
2401	ATAGCTAGAATCTTTCTGAT SEQ ID NO:1658	-6.1	-19.4	60.8	-12.4	-0.7	-6.8
2477	TTTAGAAACATATTGTCTTC SEQ ID NO:1659	-6.1	-16.8	54.7	-9.8	-0.7	-4.3
2508	TGAATGAAGTATGGTGAAAC SEQ ID NO:1660	-6.1	-16.5	52.5	-10.4	0	-3.9
2753	CCTACAGATAATAGACAACA SEQ ID NO:1661	-6.1	-18.5	56.3	-12.4	0	-2.4
2836	GTGCTATAAAATTGTGCAAA SEQ ID NO:1662	-6.1	-17.6	54.5	-10.6	-0.8	-6.1
2886	AATTTAAAATCATATTGTCA SEQ ID NO:1663	-6.1	-14.3	48.3	-8.2	0	-5
59	GGGATCGGGGGTGCACACAC SEQ ID NO:1664	-6	-28.7	78.6	-21.2	-1.3	-9.8
135	TGGTAGTTTAAGTAAGCAAA SEQ ID NO:1665	-6	-17.8	56.2	-11.8	0	-4.1
136	ATGGTAGTTTAAGTAAGCAA SEQ ID NO:1666	-6	-18.5	58.1	-12.5	0	-4.1
256	TTCCCAATCTTTATCATTGC SEQ ID NO:1667	-6	-22.7	66.7	-16.2	-0.1	-3.4
575	ACTTAACGAGCTTGGCAATT SEQ ID NO:1668	-6	-21.7	62.9	-14.8	-0.7	-6.5
674	TTTTAAACACAAGTGCAAAA SEQ ID NO:1669	-6	-15.3	49.5	-9.3	0	-5.8
732	CCAATCAACAGAGGGCTACC SEQ ID NO:1670	-6	-24.9	69.3	-18.4	-0.2	-3.7
891	GCATCAGAAGCAAAGTAATA SEQ ID NO:1671	-6	-18.5	56.8	-12	-0.1	-5.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1162	CAAATTCACAGTATAGTCAT SEQ ID NO:1672	-6	-18.3	57.6	-12.3	0	-3.1
1262	CTTGACGTGTTGCTACACCA SEQ ID NO:1673	-6	-25.3	71.2	-17.2	-2.1	-5.6
1438	CCCCACAGTTAAAGCTCCTC SEQ ID NO:1674	-6	-27.6	75.3	-21.6	0	-5
1439	TCCCCACAGTTAAAGCTCCT SEQ ID NO:1675	-6	-27.6	75.3	-21.6	0	-5
1917	GCATTCTGACACTTGGCATA SEQ ID NO:1676	-6	-24	70	-18	0	-4.2
2022	GAGTGGGGCACCTTGATCGT SEQ ID NO:1677	-6	-28.1	78.3	-20.5	-1.2	-10.7
2334	TGGGAAAATGTAAGAGGTAA SEQ ID NO:1678	-6	-17.1	53.6	-11.1	0	-1.2
2455	AGATTGAAGTGGAGGGTCCA SEQ ID NO:1679	-6	-24.3	71	-16.6	-1.7	-6.1
2955	TAAAAAACACTTTTAGGAGA SEQ ID NO:1680	-6	-14.6	48.5	-7.8	-0.6	-3.2
197	ACTCCAGTCTCTGAAGGCCT SEQ ID NO:1681	-5.9	-27.8	79.2	-21.2	-0.3	-8.5
569	CGAGCTTGGCAATTGTCTCT SEQ ID NO:1682	-5.9	-25.1	72	-18.3	-0.7	-8.3
596	TTTCCCGATTGTCATACATA SEQ ID NO:1683	-5.9	-22.7	65.7	-16.8	0	-4.4
652	ACCTTCCAATTGTTGGATAA SEQ ID NO:1684	-5.9	-21.8	63.4	-13.2	-2.7	-8.2
673	TTTAAACACAAGTGCAAAAG SEQ ID NO:1685	-5.9	-15.2	49.3	-9.3	0	-5.8
770	GAATGTGATCAGTAGAAAGT SEQ ID NO:1686	-5.9	-18.1	57.1	-12.2	0	-6.1
892	TGCATCAGAAGCAAAGTAAT SEQ ID NO:1687	-5.9	-18.8	57.3	-12	-0.8	-6.6
946	AACATCATCATCTTCCAGAA SEQ ID NO:1688	-5.9	-20.8	62.2	-14.9	0	-2.9
1338	AAGACTGGTGTGTTTCTGTC SEQ ID NO:1689	-5.9	-22.9	70.7	-16.4	-0.3	-4
1710	TGATAAAGTTCTGTTGCTAG SEQ ID NO:1690	-5.9	-19.2	60.1	-13.3	0	-3.6
1711	ATGATAAAGTTCTGTTGCTA SEQ ID NO:1691	-5.9	-19.2	59.9	-13.3	0	-3.6
1735	TCCCATTATCAGAACTGACT SEQ ID NO:1692	-5.9	-22.7	65.9	-16.3	-0.1	-7.6
1869	ACAGGCATCAATTTATCCAC SEQ ID NO:1693	-5.9	-22.2	65.2	-16.3	0	-4
1870	CACAGGCATCAATTTATCCA SEQ ID NO:1694	-5.9	-22.7	65.8	-16.8	0	-3.4
2105	CATCATAGCCTCTCAGCACA SEQ ID NO:1695	-5.9	-26	74.9	-19.2	-0.7	-4.1
2502	AAGTATGGTGAAACAAGTAC SEQ ID NO:1696	-5.9	-17.1	54.2	-10.2	-0.9	-4.9
2550	GCTTTAGATACTCCAATTAA SEQ ID NO:1697	-5.9	-19.5	59.4	-13.6	0	-2.8
2623	ATAAATCACATCTTCTCTTA SEQ ID NO:1698	-5.9	-18.1	57.5	-12.2	0	-1.5
2783	TGTAATATTTCGCTTCCTAA SEQ ID NO:1699	-5.9	-20.4	61	-14.5	0	-4.2
2788	ACTACTGTAATATTTCGCTT SEQ ID NO:1700	-5.9	-20	60.9	-14.1	0	-4.2
508	AAACTTTTTCAAGTCTTTGT SEQ ID NO:1701	-5.8	-18.4	58.3	-11.2	-1.3	-4.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
703	GCCAACTGCTTGCCCGGGAA SEQ ID NO:1702	-5.8	-30.6	78	-23.2	-0.2	-11.4
728	TCAACAGAGGGCTACCTCGC SEQ ID NO:1703	-5.8	-26.8	74.5	-17.1	-3.9	-9.6
912	GTGTGTTCTATGACAGCACT SEQ ID NO:1704	-5.8	-23.8	71.9	-16.4	-1.6	-5.8
916	ATTGGTGTGTTCTATGACAG SEQ ID NO:1705	-5.8	-21.5	66.3	-15.2	-0.1	-3.9
1078	CATAAATGAACTGAAGTTGC SEQ ID NO:1706	-5.8	-17	53.3	-11.2	0	-5.7
1222	AGCAATAAGAATCAAACGCC SEQ ID NO:1707	-5.8	-19.2	56.2	-13.4	0	-4.1
1285	CAACTCAGTCAGCTCCTCAA SEQ ID NO:1708	-5.8	-24.9	72.2	-19.1	0	-4.4
1503	CCAGCATTAATATGAACTCC SEQ ID NO:1709	-5.8	-21.4	62.2	-14.9	-0.4	-4.2
1505	GACCAGCATTAATATGAACT SEQ ID NO:1710	-5.8	-19.8	59.1	-13.3	-0.4	-4.2
1507	AGGACCAGCATTAATATGAA SEQ ID NO:1711	-5.8	-19.9	59.3	-13.4	-0.4	-4.2
1749	TAATGATAGCCTCGTCCCAT SEQ ID NO:1712	-5.8	-25.5	70.5	-19.7	0	-3.2
1751	CATAATGATAGCCTCGTCCC SEQ ID NO:1713	-5.8	-25.5	70.5	-19.7	0	-3.2
2089	CACAGCAAGGTGGAAAGCCA SEQ ID NO:1715	-5.8	-24.7	68.6	-17.5	-1.3	-6.6
2102	CATAGCCTCTCAGCACAGCA SEQ ID NO:1715	-5.8	-27.4	78	-20.7	-0.7	-4.8
2223	ATCAAGGTTTTAAATACAAA SEQ ID NO:1716	-5.8	-14.6	48.6	-8.8	0	-5.4
2294	GAGTGGAATAATTATAACTG SEQ ID NO:1717	-5.8	-15.8	51.4	-10	0	-6.3
2496	GGTGAAACAAGTACCAATTT SEQ ID NO:1718	-5.8	-19.1	57.4	-12.3	-0.9	-5.3
2759	CTTCCACCTACAGATAATAG SEQ ID NO:1719	-5.8	-21.1	62.4	-15.3	0	-2.1
2827	AATTGTGCAAATATGTTAAG SEQ ID NO:1720	-5.8	-15.7	51	-9.9	0	-6.1
2840	GTTTGTGCTATAAAATTGTG SEQ ID NO:1721	-5.8	-17.9	56.4	-12.1	0	-3.6
2908	ACATGTACACATCCCATCTT SEQ ID NO:1722	-5.8	-24.1	69.4	-18.3	0	-6.7
123	TAAGCAAATATACCACACAT SEQ ID NO:1723	-5.7	-18.2	55.1	-12.5	0	-4.1
202	TCTGTACTCCAGTCTCTGAA SEQ ID NO:1724	-5.7	-24.1	72.5	-17.5	-0.8	-5.2
301	AACTTTTCCTTTCTTCTTAA SEQ ID NO:1725	-5.7	-20	61.8	-14.3	0	-2
512	CCAAAAACTTTTTCAAGTCT SEQ ID NO:1726	-5.7	-18.3	56	-11.2	-1.3	-4.9
961	ATCCACTACTGCTGCAACAT SEQ ID NO:1727	-5.7	-24.4	69.3	-18.7	0	-7.3
1165	ACCCAAATTCACAGTATAGT SEQ ID NO:1728	-5.7	-21.4	63.1	-15.7	0	-2.7
1236	TAACTTGTTCCACAAGCAAT SEQ ID NO:1729	-5.7	-20.6	60.9	-12	-2.9	-8.2
1237	GTAACTTGTTCCACAAGCAA SEQ ID NO:1730	-5.7	-21.8	63.9	-13.2	-2.9	-8.2
1651	CAAATCAGGCAGCCGTTTCA SEQ ID NO:1731	-5.7	-25.2	70.2	-18.7	-0.3	-9

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1864	CATCAATTTATCCACCAAAG SEQ ID NO:1732	-5.7	-19.6	58	-13.9	0	-2.6
2072	CCAGCAACTGTAAAGGGATC SEQ ID NO:1733	-5.7	-22.5	64.9	-15.4	-1.3	-6.4
2077	GAAAGCCAGCAACTGTAAAG SEQ ID NO:1734	-5.7	-20.1	59	-13.4	-0.9	-6.4
2187	TTAATCATACAGTTTCGTAC SEQ ID NO:1735	-5.7	-18.5	58.1	-12.8	0	-3.4
2770	TTCCTAAATTTCTTCCACCT SEQ ID NO:1736	-5.7	-23.5	67.4	-17.8	0	-4.6
2966	ATACAAGGAAATAAAAAACA SEQ ID NO:1737	-5.7	-11.4	41.9	-5.7	0	-1.2
67	TGGCTGGCGGGATCGGGGGT SEQ ID NO:1738	-5.6	-31.9	84.3	-25.4	-0.7	-6.3
296	TTCCTTTCTTCTTAATAAGC SEQ ID NO:1739	-5.6	-20.2	62.3	-14.6	0	-5.1
595	TTCCCGATTGTCATACATAT SEQ ID NO:1740	-5.6	-22.6	65.3	-17	0	-3.9
966	CGTCCATCCACTACTGCTGC SEQ ID NO:1741	-5.6	-28.6	78.3	-23	0	-5
1731	ATTATCAGAACTGACTTCTG SEQ ID NO:1742	-5.6	-19	59.3	-11.6	-1.8	-7.6
1902	GCATAAGTGTGATCTCTCAT SEQ ID NO:1743	-5.6	-22.2	67.7	-15.9	-0.4	-6.5
1912	CTGACACTTGGCATAAGTGT SEQ ID NO:1744	-5.6	-22.7	67.1	-12.9	-4.2	-11.2
2175	TTTCGTACATTTTGTATAGA SEQ ID NO:1745	-5.6	-18.7	58.9	-12.5	-0.3	-4.8
2338	TTACTGGGAAAATGTAAGAG SEQ ID NO:1746	-5.6	-16.6	52.8	-11	0	-3.7
2473	GAAACATATTGTCTTCTCAG SEQ ID NO:1747	-5.6	-18.9	59.3	-12.4	-0.7	-4.3
2481	AATTTTTAGAAACATATTGT SEQ ID NO:1748	-5.6	-14.5	48.9	-8.9	0	-2.9
2534	TTAAATGCACTACTCTTTCA SEQ ID NO:1749	-5.6	-19.4	59.7	-13.8	0	-5
2603	AAACTTGGCAAACCCTTCCC SEQ ID NO:1750	-5.6	-25.7	68.5	-19.4	-0.5	-4
568	GAGCTTGGCAATTGTCTCTG SEQ ID NO:1751	-5.5	-24.3	71.9	-17.9	-0.7	-8.3
584	CATACATATACTTAACGAGC SEQ ID NO:1752	-5.5	-18.3	56.2	-12.8	0	-3.5
651	CCTTCCAATTGTTGGATAAC SEQ ID NO:1753	-5.5	-21.8	63.4	-13.6	-2.7	-8.2
702	CCAACTGCTTGCCCGGGAAA SEQ ID NO:1754	-5.5	-28.1	72.1	-21	0	-11.4
941	CATCATCTTCCAGAAAGATG SEQ ID NO:1755	-5.5	-20.1	60.5	-11	-3.6	-8.8
1617	TCTTTGCGTCTTTCTTGCAT SEQ ID NO:1756	-5.5	-24.7	73	-18.2	-0.9	-5.1
1924	CTGAAGAGCATTCTGACACT SEQ ID NO:1757	-5.5	-21.9	65.1	-15.4	-0.9	-5.2
2138	TCACAGATTTGGCAAGATTC SEQ ID NO:1758	-5.5	-20.9	63.4	-15.4	0	-4
2166	TTTTGTATAGATATTCCTCA SEQ ID NO:1759	-5.5	-19.7	61.7	-14.2	0	-2.8
2222	TCAAGGTTTTAAATACAAAA SEQ ID NO:1760	-5.5	-13.9	47.1	-8.4	0	-4.6
2361	CATTATTCAAAGTCCTCCAC SEQ ID NO:1761	-5.5	-22.1	64.9	-16.6	0	-1.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2400	TAGCTAGAATCTTTCTGATA SEQ ID NO:1762	-5.5	-19.1	60.3	-12.9	-0.4	-6.6
2445	GGAGGGTCCAGAAATGCAAC SEQ ID NO:1763	-5.5	-23.7	67.3	-17.3	-0.8	-7.2
2661	CAGTTTGATTTAAAAACAAA SEQ ID NO:1764	-5.5	-13.3	45.8	-6.1	-1.7	-9
2914	TACCCAACATGTACACATCC SEQ ID NO:1765	-5.5	-23.9	67	-18.4	0	-7
61	GCGGGATCGGGGGTGCACAC SEQ ID NO:1766	-5.4	-30.4	80.8	-23.4	-0.7	-11.1
668	ACACAAGTGCAAAAGCACCT SEQ ID NO:1767	-5.4	-22.3	63.2	-14.5	-2.4	-9
960	TCCACTACTGCTGCAACATC SEQ ID NO:1768	-5.4	-24.8	70.9	-19.4	0	-7.3
1028	GTGTTTGCACAGCTCGTCCG SEQ ID NO:1769	-5.4	-28.3	78.6	-21	-1.9	-8.4
1419	CTCTCCTTACAGTAACGAAG SEQ ID NO:1770	-5.4	-21.3	62.8	-15.9	0	-4.7
1706	AAAGTTCTGTTGCTAGTTTC SEQ ID NO:1771	-5.4	-20.7	65	-15.3	0	-4.1
1817	CAAGGATGCCTTCAGAGTGC SEQ ID NO:1772	-5.4	-25.3	72.8	-18.7	-1.1	-5.5
2094	CTCAGCACAGCAAGGTGGAA SEQ ID NO:1773	-5.4	-24.7	70.7	-18.4	-0.7	-5.5
2272	ATATAAATAAGGATTTACTA SEQ ID NO:1774	-5.4	-13.5	46.8	-6.7	-1.3	-4.1
2476	TTAGAAACATATTGTCTTCT SEQ ID NO:1775	-5.4	-17.6	56.3	-10.6	-1.5	-5.9
2497	TGGTGAAACAAGTACCAATT SEQ ID NO:1776	-5.4	-19	57	-12.3	-1.2	-5.6
2597	GGCAAACCCTTCCCTAACTG SEQ ID NO:1777	-5.4	-26.9	71.4	-21.5	0	-4
2841	AGTTTGTGCTATAAAATTGT SEQ ID NO:1778	-5.4	-17.9	56.6	-12.5	0	-3.6
41	ACGAGCTTCGGTGGGCAATC SEQ ID NO:1779	-5.3	-26.6	73.6	-19.8	-1.4	-7.3
48	TGCACACACGAGCTTCGGTG SEQ ID NO:1780	-5.3	-26.3	72.5	-18.2	-2.8	-10.4
962	CATCCACTACTGCTGCAACA SEQ ID NO:1781	-5.3	-25.1	70.4	-19.8	0	-7.3
1398	CCCATCAAAGTATCTGCTGT SEQ ID NO:1782	-5.3	-24.5	70	-19.2	0	-3.6
1426	AGCTCCTCTCTCCTTACAGT SEQ ID NO:1783	-5.3	-27.8	81.9	-22.5	0	-4.3
1490	GAACTCCACAATCTGTCTCC SEQ ID NO:1784	-5.3	-24.5	70.5	-19.2	0	-2.6
1652	TCAAATCAGGCAGCCGTTTC SEQ ID NO:1785	-5.3	-24.9	70.6	-18.8	-0.3	-9
1689	TTCTGAATTTCGTCATCCAT SEQ ID NO:1786	-5.3	-22.1	65.3	-16.8	0	-5
1859	ATTTATCCACCAAAGCCAGA SEQ ID NO:1787	-5.3	-23.6	66.2	-18.3	0	-3.2
2016	GGCACCTTGATCGTTCTTTT SEQ ID NO:1788	-5.3	-25.6	73.4	-20.3	0	-5.3
2140	AGTCACAGATTTGGCAAGAT SEQ ID NO:1789	-5.3	-21.6	65	-16.3	0	-4.1
2407	AAAATAATAGCTAGAATCTT SEQ ID NO:1790	-5.3	-14.3	48.2	-9	0	-6.3
2547	TTAGATACTCCAATTAAATG SEQ ID NO:1791	-5.3	-16	51.5	-10.7	0	-3.2

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2817	ATATGTTAAGGATTGAGACC SEQ ID NO:1792	-5.3	-19.3	59.3	-14	0	-3.2
2902	ACACATCCCATCTTCAAATT SEQ ID NO:1793	-5.3	-22.1	63.9	-16.8	0	-2.9
2903	TACACATCCCATCTTCAAAT SEQ ID NO:1794	-5.3	-21.7	63	-16.4	0	-1
2974	GACTACAGATACAAGGAAAT SEQ ID NO:1795	-5.3	-17.2	53.9	-11.9	0	-2.2
2975	AGACTACAGATACAAGGAAA SEQ ID NO:1796	-5.3	-17.2	54	-11.9	0	-2.2
473	CATTGTGAATAACGATAAAT SEQ ID NO:1797	-5.2	-14.8	48.3	-9	-0.3	-3.5
513	TCCAAAAACTTTTTCAAGTC SEQ ID NO:1798	-5.2	-17.8	55.4	-11.2	-1.3	-4.9
893	TTGCATCAGAAGCAAAGTAA SEQ ID NO:1799	-5.2	-18.9	57.6	-12	-1.7	-8.5
930	AGAAAGATGACGCGATTGGT SEQ ID NO:1800	-5.2	-21.1	60.7	-15.4	0	-7.9
1173	TTCAAACCACCCAAATTCAC SEQ ID NO:1801	-5.2	-21.6	61	-16.4	0	-3.1
1414	CTTACAGTAACGAAGACCCA SEQ ID NO:1802	-5.2	-22.2	62.9	-17	0	-4.7
1729	TATCAGAACTGACTTCTGAT SEQ ID NO:1803	-5.2	-19.5	60.3	-10	-4.3	-10.1
1758	CAAGTAGCATAATGATAGCC SEQ ID NO:1804	-5.2	-20.5	61.3	-14.8	-0.1	-4.1
1821	CCAGCAAGGATGCCTTCAGA SEQ ID NO:1805	-5.2	-26.8	74.3	-19.4	-2.2	-6.5
1857	TTATCCACCAAAGCCAGAGG SEQ ID NO:1806	-5.2	-24.7	68.5	-19.5	0	-3.6
1858	TTTATCCACCAAAGCCAGAG SEQ ID NO:1807	-5.2	-23.6	66.5	-18.4	0	-3.2
1953	ACAGGCCGCCCCTGCCGAGC SEQ ID NO:1808	-5.2	-36.4	88.6	-28.4	-2.8	-9
2092	CAGCACAGCAAGGTGGAAAG SEQ ID NO:1809	-5.2	-22.7	65.4	-16.6	-0.7	-5.5
2129	TGGCAAGATTCCGTGGGAAA SEQ ID NO:1810	-5.2	-23.7	65.9	-17	-1.4	-6.8
2303	TCACATATTGAGTGGAATAA SEQ ID NO:1811	-5.2	-17.7	55.6	-11.6	-0.7	-4.7
2319	GGTAACTTCACAAAAATCAC SEQ ID NO:1812	-5.2	-17.1	53.6	-11.9	0	-2.7
2354	CAAAGTCCTCCACAAATTAC SEQ ID NO:1813	-5.2	-20.4	59.8	-15.2	0	-3.3
2505	ATGAAGTATGGTGAAACAAG SEQ ID NO:1815	-5.2	-16.6	52.7	-10.4	-0.9	-3.9
2785	ACTGTAATATTTCGCTTCCT SEQ ID NO:1815	-5.2	-22.5	66.1	-17.3	0	-3.9
2916	GATACCCAACATGTACACAT SEQ ID NO:1816	-5.2	-22.1	63.4	-16.9	0	-7
196	CTCCAGTCTCTGAAGGCCTT SEQ ID NO:1817	-5.1	-27.7	79	-21.2	-0.3	-10.8
342	TCCATATCTTGTTGCTTGTG SEQ ID NO:1818	-5.1	-23.5	70.4	-18.4	0	-3.6
514	TTCCAAAAACTTTTTCAAGT SEQ ID NO:1819	-5.1	-17.5	54.5	-11.2	-1.1	-4.9
565	CTTGGCAATTGTCTCTGTGT SEQ ID NO:1820	-5.1	-24.3	72.6	-18.7	0	-8.3
667	CACAAGTGCAAAAGCACCTT SEQ ID NO:1821	-5.1	-22.2	63	-15.5	-1.6	-8.2

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
799	CTTGTCTTTGCCTGTTCTGT SEQ ID NO:1822	-5.1	-26.2	78.2	-21.1	0	-3
811	GCAGCTTCCTTTCTTGTCTT SEQ ID NO:1823	-5.1	-26.8	79.8	-21.7	0	-4.5
814	ATTGCAGCTTCCTTTCTTGT SEQ ID NO:1824	-5.1	-25.5	75.5	-20.4	0	-5.2
1117	GTTCACGACAGACTCTGGCT SEQ ID NO:1825	-5.1	-25.8	74.2	-19.8	-0.7	-6.8
1182	ATGTGATCCTTCAAACCACC SEQ ID NO:1826	-5.1	-24	67.5	-18.2	-0.5	-4.3
1440	ATCCCCACAGTTAAAGCTCC SEQ ID NO:1827	-5.1	-26.7	73.4	-21.6	0	-5
1442	TGATCCCCACAGTTAAAGCT SEQ ID NO:1828	-5.1	-24.9	69.5	-19.8	0	-4.8
1737	CGTCCCATTATCAGAACTGA SEQ ID NO:1829	-5.1	-23.6	66.8	-18.5	0	-7.3
2021	AGTGGGGCACCTTGATCGTT SEQ ID NO:1830	-5.1	-27.6	77.4	-20.5	-2	-10.7
2056	GATCACGCTGAGAATGCCCT SEQ ID NO:1831	-5.1	-26.6	72.2	-21	-0.1	-5.1
2061	AAAGGGATCACGCTGAGAAT SEQ ID NO:1832	-5.1	-20.9	60.7	-15.3	-0.1	-5.1
2626	AAAATAAATCACATCTTCTC SEQ ID NO:1833	-5.1	-15.3	50.4	-10.2	0	-1.2
2704	AGATATAAATCCTACCAATA SEQ ID NO:1834	-5.1	-17.5	54.1	-11.6	-0.6	-2.7
2766	TAAATTTCTTCCACCTACAG SEQ ID NO:1835	-5.1	-20.7	61.5	-15.6	0	-4.9
2825	TTGTGCAAATATGTTAAGGA SEQ ID NO:1836	-5.1	-18.2	56.5	-13.1	0	-5.4
2835	TGCTATAAAATTGTGCAAAT SEQ ID NO:1837	-5.1	-16.4	51.8	-10.6	-0.4	-6.1
2882	TAAAATCATATTGTCAGTTG SEQ ID NO:1838	-5.1	-16.1	52.6	-11	0	-2.1
2904	GTACACATCCCATCTTCAAA SEQ ID NO:1839	-5.1	-22.9	66.1	-17.8	0	-4.6
2973	ACTACAGATACAAGGAAATA SEQ ID NO:1840	-5.1	-16.3	52.1	-11.2	0	-2.2
148	CGTTCGAGGAACATGGTAGT SEQ ID NO:1841	-5	-23.2	66.8	-16.3	-1.9	-6.7
371	CAAGGTGTACATCAAATTCT SEQ ID NO:1842	-5	-19.3	59.2	-13.8	0	-7.9
570	ACGAGCTTGGCAATTGTCTC SEQ ID NO:1843	-5	-24.4	70.7	-18.5	-0.7	-8.3
831	CTGTCCACACGAGAGAGATT SEQ ID NO:1844	-5	-23.6	68.1	-18.6	0	-3.5
840	CAGGTTGTGCTGTCCACACG SEQ ID NO:1845	-5	-27.3	76.5	-20.4	-1.9	-7
1031	GGAGTGTTTGCACAGCTCGT SEQ ID NO:1846	-5	-26.9	78	-19.1	-2.8	-9.1
1104	TCTGGCTGCTCAAATATTTC SEQ ID NO:1847	-5	-21.9	65.7	-16.9	0	-6.1
1181	TGTGATCCTTCAAACCACCC SEQ ID NO:1848	-5	-26	70.9	-20.3	-0.5	-4.3
1187	CCTTTATGTGATCCTTCAAA SEQ ID NO:1849	-5	-21.7	63.7	-16	-0.5	-5.5
1545	TGGCTGGTATAAGCCTTTGT SEQ ID NO:1850	-5	-25.1	72.7	-16.9	-3.2	-9.5
1680	TCGTCATCCATGCTCAGTAC SEQ ID NO:1851	-5	-25.5	74.3	-20.5	0	-4.2

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1744	ATAGCCTCGTCCCATTATCA SEQ ID NO:1852	-5	-26.8	74.6	-21.8	0	-3.2
1888	TCTCATGATGATCATGATCA SEQ ID NO:1853	-5	-20.4	62.6	-11.9	-3.5	-13.9
2088	ACAGCAAGGTGGAAAGCCAG SEQ ID NO:1854	-5	-24	67.8	-17.5	-1.4	-6.6
2398	GCTAGAATCTTTCTGATACA SEQ ID NO:1855	-5	-20.3	62.5	-14.4	-0.7	-6.3
2498	ATGGTGAAACAAGTACCAAT SEQ ID NO:1856	-5	-18.9	56.7	-12.3	-1.6	-6.5
2500	GTATGGTGAAACAAGTACCA SEQ ID NO:1857	-5	-20.5	60.9	-14	-1.4	-6.1
2613	TCTTCTCTTAAAACTTGGCA SEQ ID NO:1858	-5	-20.6	62.3	-15.6	0	-4
2733	AGTCTGAGAAACTAAGGCTA SEQ ID NO:1859	-5	-20	61.1	-15	0	-3.7
2787	CTACTGTAATATTTCGCTTC SEQ ID NO:1860	-5	-20.2	61.7	-15.2	0	-4.2
2798	CCACCAATGCACTACTGTAA SEQ ID NO:1861	-5	-23.5	65.9	-18.5	0	-5.5
2888	CAAATTTAAAATCATATTGT SEQ ID NO:1862	-5	-13.2	45.8	-8.2	0	-5
2956	ATAAAAAACACTTTTAGGAG SEQ ID NO:1863	-5	-14	47.3	-7.8	-1.1	-3.6
38	AGCTTCGGTGGGCAATCTGC SEQ ID NO:1864	-4.9	-27.7	77.9	-21.6	-1.1	-6.5
649	TTCCAATTGTTGGATAACTC SEQ ID NO:1865	-4.9	-20.2	61.1	-12.6	-2.7	-8.2
765	TGATCAGTAGAAAGTTTATG SEQ ID NO:1866	-4.9	-16.9	54.8	-12	0	-6
956	CTACTGCTGCAACATCATCA SEQ ID NO:1867	-4.9	-23.3	67.8	-18.4	0	-7.3
1025	TTTGCACAGCTCGTCCGGGG SEQ ID NO:1868	-4.9	-29.5	79.6	-24	-0.3	-6.9
1106	ACTCTGGCTGCTCAAATATT SEQ ID NO:1869	-4.9	-22.5	66.3	-17.6	0	-6.1
1171	CAAACCACCCAAATTCACAG SEQ ID NO:1870	-4.9	-21.8	60.7	-16.9	0	-3.1
1234	ACTTGTTCCACAAGCAATAA SEQ ID NO:1871	-4.9	-20.6	60.9	-12.8	-2.9	-8.2
1279	AGTCAGCTCCTCAAGAACTT SEQ ID NO:1872	-4.9	-23.8	70.3	-18.9	0	-4.4
1411	ACAGTAACGAAGACCCATCA SEQ ID NO:1873	-4.9	-22.6	63.7	-17	-0.4	-3.9
1681	TTCGTCATCCATGCTCAGTA SEQ ID NO:1874	-4.9	-25.4	74.1	-20.5	0	-4.2
1701	TCTGTTGCTAGTTTCTGAAT SEQ ID NO:1875	-4.9	-21.6	66.7	-16.7	0	-4.7
1730	TTATCAGAACTGACTTCTGA SEQ ID NO:1876	-4.9	-19.6	60.7	-11.1	-3.6	-8.7
1738	TCGTCCCATTATCAGAACTG SEQ ID NO:1877	-4.9	-23.4	67	-18.5	0	-4.9
2125	AAGATTCCGTGGGAAATCAA SEQ ID NO:1878	-4.9	-20.4	59.3	-13.6	-1.9	-7.1
2172	CGTACATTTTGTATAGATAT SEQ ID NO:1879	-4.9	-17.8	56.3	-12	-0.8	-4.8
2461	CTTCTCAGATTGAAGTGGAG SEQ ID NO:1880	-4.9	-21	64.5	-15.3	-0.6	-4.7
2621	AAATCACATCTTCTCTTAAA SEQ ID NO:1881	-4.9	-17	54.3	-12.1	0	-2.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2790	GCACTACTGTAATATTTCGC SEQ ID NO:1882	-4.9	-21.5	63.9	-16.6	0	-6.8
105	ATGATGCCGGAGACACGGCC SEQ ID NO:1883	-4.8	-28.5	74.5	-20.3	-3.4	-9.9
254	CCCAATCTTTATCATTGCCT SEQ ID NO:1884	-4.8	-25.1	70.3	-19.8	-0.1	-3.4
431	GGGGGTGGCTATTGACAGGA SEQ ID NO:1885	-4.8	-27	77.1	-22.2	0	-3.7
838	GGTTGTGCTGTCCACACGAG SEQ ID NO:1886	-4.8	-27.2	76.8	-20.4	-2	-7.2
839	AGGTTGTGCTGTCCACACGA SEQ ID NO:1887	-4.8	-27.2	76.8	-20.4	-2	-7.2
980	GATGGATAGAAAGACGTCCA SEQ ID NO:1888	-4.8	-21.2	61.7	-15.1	-1.2	-8.6
1105	CTCTGGCTGCTCAAATATTT SEQ ID NO:1889	-4.8	-22.4	66.1	-17.6	0	-5.8
1459	ACTGCCAACTGTGTTTGTGA SEQ ID NO:1890	-4.8	-24.4	70.8	-19.6	0	-3.3
1969	CTTATCACAAATTACCACAG SEQ ID NO:1891	-4.8	-18.9	57.3	-14.1	0	-3.2
2576	CCAAGTATGAGCATACACTG SEQ ID NO:1892	-4.8	-21.7	63.7	-15.4	-1.4	-9.6
2705	TAGATATAAATCCTACCAAT SEQ ID NO:1893	-4.8	-17.5	54.1	-11.9	-0.6	-2.7
2948	CACTTTTAGGAGATGAAAAC SEQ ID NO:1894	-4.8	-16.9	53.5	-12.1	0	-3
3035	GTGTTGTGATTTTAAAGAAC SEQ ID NO:1895	-4.8	-17	54.7	-12.2	0	-4.6
69	AGTGGCTGGCGGGATCGGGG SEQ ID NO:1896	-4.7	-30.7	82.1	-25.1	-0.7	-6.3
147	GTTCGAGGAACATGGTAGTT SEQ ID NO:1897	-4.7	-22.5	66.9	-16.3	-1.4	-6.5
515	TTTCCAAAAACTTTTTCAAG SEQ ID NO:1898	-4.7	-16.4	52.1	-11.2	-0.1	-4.7
1679	CGTCATCCATGCTCAGTACT SEQ ID NO:1899	-4.7	-26	74.6	-21.3	0	-5.5
1704	AGTTCTGTTGCTAGTTTCTG SEQ ID NO:1900	-4.7	-23	72.2	-18.3	0	-4.1
1707	TAAAGTTCTGTTGCTAGTTT SEQ ID NO:1901	-4.7	-20	62.8	-15.3	0	-4.1
2014	CACCTTGATCGTTCTTTTTG SEQ ID NO:1902	-4.7	-22.7	66.8	-18	0	-5.3
2167	ATTTTGTATAGATATTCCTC SEQ ID NO:1903	-4.7	-19	60.3	-14.3	0	-2.8
2360	ATTATTCAAAGTCCTCCACA SEQ ID NO:1904	-4.7	-22.1	64.9	-17.4	0	-2.5
2499	TATGGTGAAACAAGTACCAA SEQ ID NO:1905	-4.7	-18.6	56.2	-12.3	-1.6	-6.5
2658	TTTGATTTAAAAACAAAACA SEQ ID NO:1906	-4.7	-11.6	42.4	-6.4	0.2	-8.4
2887	AAATTTAAAATCATATTGTC SEQ ID NO:1907	-4.7	-12.9	45.5	-8.2	0	-5
2979	TAAAAGACTACAGATACAAG SEQ ID NO:1908	-4.7	-14.4	48.2	-9.7	0	-2.2
2980	ATAAAAGACTACAGATACAA SEQ ID NO:1909	-4.7	-14.4	48.1	-9.7	0	-2.2
2981	AATAAAAGACTACAGATACA SEQ ID NO:1910	-4.7	-14.4	48.1	-9.7	0	-2.2
1207	ACGCCGGCATCTCTGGATCT SEQ ID NO:1911	-4.6	-29	78.3	-22.8	-0.9	-11.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1540	GGTATAAGCCTTTGTACTGG SEQ ID NO:1912	-4.6	-23.2	68.5	-17.3	-1.2	-5.4
1571	GGGCAAACATCACAAGGGAT SEQ ID NO:1913	-4.6	-22.7	64.6	-18.1	0	-4
1947	CGCCCCTGCCGAGCAACCAC SEQ ID NO:1915	-4.6	-33.6	81.3	-28.1	-0.7	-7.1
2454	GATTGAAGTGGAGGGTCCAG SEQ ID NO:1915	-4.6	-24.3	71	-17.8	-1.9	-6.2
2655	GATTTAAAAACAAAACAGAA SEQ ID NO:1916	-4.6	-11.3	41.8	-6.7	0	-5
2659	GTTTGATTTAAAAACAAAAC SEQ ID NO:1917	-4.6	-12.1	43.5	-6.4	-0.9	-9.2
2786	TACTGTAATATTTCGCTTCC SEQ ID NO:1918	-4.6	-21.3	63.6	-16.7	0	-4.2
2831	ATAAAATTGTGCAAATATGT SEQ ID NO:1919	-4.6	-14.9	49	-10.3	0	-6.1
3036	TGTGTTGTGATTTTAAAGAA SEQ ID NO:1920	-4.6	-16.8	54.1	-12.2	0	-4.6
829	GTCCACACGAGAGAGATTGC SEQ ID NO:1921	-4.5	-24.5	70.3	-20	0	-3.5
963	CCATCCACTACTGCTGCAAC SEQ ID NO:1922	-4.5	-26.4	72.8	-21.9	0	-7.3
1335	ACTGGTGTGTTTCTGTCCAG SEQ ID NO:1923	-4.5	-25.7	77.1	-19.3	-1.9	-6.5
1406	AACGAAGACCCATCAAAGTA SEQ ID NO:1924	-4.5	-20.3	58.5	-15.1	-0.4	-3.9
1743	TAGCCTCGTCCCATTATCAG SEQ ID NO:1925	-4.5	-26.8	75	-22.3	0	-3.2
1826	ATTCACCAGCAAGGATGCCT SEQ ID NO:1926	-4.5	-26.4	73.3	-19.7	-2.2	-5.9
2168	CATTTTGTATAGATATTCCT SEQ ID NO:1927	-4.5	-19.3	60.2	-14.8	0	-2.8
2355	TCAAAGTCCTCCACAAATTA SEQ ID NO:1928	-4.5	-20.6	60.6	-16.1	0	-3.3
2546	TAGATACTCCAATTAAATGC SEQ ID NO:1929	-4.5	-17.7	55	-13.2	0	-3.5
2942	TAGGAGATGAAAACACAAAG SEQ ID NO:1930	-4.5	-15	48.9	-10.5	0	-2.5
2976	AAGACTACAGATACAAGGAA SEQ ID NO:1931	-4.5	-17.2	54	-12.7	0	-2.2
60	CGGGATCGGGGGTGCACACA SEQ ID NO:1932	-4.4	-29.3	77.7	-24	0	-9.8
372	CCAAGGTGTACATCAAATTC SEQ ID NO:1933	-4.4	-20.4	61	-15.5	0	-7.9
650	CTTCCAATTGTTGGATAACT SEQ ID NO:1934	-4.4	-20.7	61.7	-13.6	-2.7	-8.2
1036	CATCTGGAGTGTTTGCACAG SEQ ID NO:1935	-4.4	-23.8	70.9	-16.7	-2.7	-7.3
1180	GTGATCCTTCAAACCACCCA SEQ ID NO:1936	-4.4	-26.7	72.1	-21.6	-0.5	-4.3
1218	ATAAGAATCAAACGCCGGCA SEQ ID NO:1937	-4.4	-21.9	60.5	-15.8	0	-11.6
1282	CTCAGTCAGCTCCTCAAGAA SEQ ID NO:1938	-4.4	-24.6	72.1	-20.2	0	-4.4
1283	ACTCAGTCAGCTCCTCAAGA SEQ ID NO:1939	-4.4	-25.5	75.3	-21.1	0	-4.4
1619	TCTCTTTGCGTCTTTCTTGC SEQ ID NO:1940	-4.4	-25.3	75.8	-20.9	0	-4
1736	GTCCCATTATCAGAACTGAC SEQ ID NO:1941	-4.4	-23	67.1	-18.1	-0.1	-7.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1836	CCATGTTTCAATTCACCAGC SEQ ID NO:1942	-4.4	-24.4	69.8	-20	0	-4.3
2273	TATATAAATAAGGATTTACT SEQ ID NO:1943	-4.4	-13.5	46.8	-7.7	-1.3	-6.3
2431	TGCAACACCCAGCATTCTTT SEQ ID NO:1944	-4.4	-25.7	71.6	-20.4	-0.8	-4.8
2504	TGAAGTATGGTGAAACAAGT SEQ ID NO:1945	-4.4	-17.8	55.5	-12.4	-0.9	-3.9
3037	CTGTGTTGTGATTTTAAAGA SEQ ID NO:1946	-4.4	-18.4	58	-14	0	-4.6
62	GGCGGGATCGGGGGTGCACA SEQ ID NO:1947	-4.3	-31.4	82.7	-25.5	-0.7	-11.1
80	GGCCAGGGGCGAGTGGCTGG SEQ ID NO:1948	-4.3	-32.8	87.5	-25.2	-3.3	-9.8
340	CATATCTTGTTGCTTGTGAA SEQ ID NO:1949	-4.3	-21	63.9	-16.7	0	-3.6
511	CAAAAACTTTTTCAAGTCTT SEQ ID NO:1950	-4.3	-16.4	52.6	-11.2	-0.8	-4.9
576	TACTTAACGAGCTTGGCAAT SEQ ID NO:1951	-4.3	-21.3	62	-16.1	-0.7	-6.5
594	TCCCGATTGTCATACATATA SEQ ID NO:1952	-4.3	-22.2	64.4	-17.9	0	-4.4
1164	CCCAAATTCACAGTATAGTC SEQ ID NO:1953	-4.3	-21.6	64	-17.3	0	-3.1
1443	GTGATCCCCACAGTTAAAGC SEQ ID NO:1954	-4.3	-25.2	70.8	-19.6	-1.2	-5.2
1653	ATCAAATCAGGCAGCCGTTT SEQ ID NO:1955	-4.3	-24.5	69.1	-19.4	-0.3	-9
1708	ATAAAGTTCTGTTGCTAGTT SEQ ID NO:1956	-4.3	-19.9	62.4	-15.6	0	-4.1
1829	TCAATTCACCAGCAAGGATG SEQ ID NO:1957	-4.3	-22.1	64.2	-17	-0.6	-4.9
1833	TGTTTCAATTCACCAGCAAG SEQ ID NO:1958	-4.3	-21.7	64.2	-17.4	0	-4.1
1894	GTGATCTCTCATGATGATCA SEQ ID NO:1959	-4.3	-21.8	66.8	-14.7	-2.7	-12.9
1964	CACAAATTACCACAGGCCGC SEQ ID NO:1960	-4.3	-25.4	68.1	-20.6	0	-7.7
2141	CAGTCACAGATTTGGCAAGA SEQ ID NO:1961	-4.3	-22.3	66.2	-18	0	-4.1
2399	AGCTAGAATCTTTCTGATAC SEQ ID NO:1962	-4.3	-19.6	61.4	-14.4	-0.7	-6.9
2442	GGGTCCAGAAATGCAACACC SEQ ID NO:1963	-4.3	-24.8	68.5	-19.4	-1	-5.6
2801	GACCCACCAATGCACTACTG SEQ ID NO:1964	-4.3	-26.1	70.7	-21.8	0	-5.5
2883	TTAAAATCATATTGTCAGTT SEQ ID NO:1965	-4.3	-16.2	52.9	-11.9	0	-2.1
2957	AATAAAAAACACTTTTAGGA SEQ ID NO:1966	-4.3	-13.3	45.8	-7.8	-1.1	-3.6
3052	AATTTAATAGCAGCTCTGTG SEQ ID NO:1967	-4.3	-19.9	61.2	-15.6	0	-6.1
146	TTCGAGGAACATGGTAGTTT SEQ ID NO:1968	-4.2	-21.4	64.1	-17.2	0	-7.2
459	ATAAATTCATTATTTTTATC SEQ ID NO:1969	-4.2	-13.8	48	-9.1	-0.2	-4.9
683	AATGAACACTTTTAAACACA SEQ ID NO:1970	-4.2	-15.6	50.2	-11.4	0	-4.4
825	ACACGAGAGAGATTGCAGCT SEQ ID NO:1971	-4.2	-23.6	68.3	-19.4	0	-5.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
905	CTATGACAGCACTTGCATCA SEQ ID NO:1972	-4.2	-23.4	68.5	-18.3	-0.7	-7.7
926	AGATGACGCGATTGGTGTGT SEQ ID NO:1973	-4.2	-24.3	69.2	-19.6	-0.1	-7.9
981	CGATGGATAGAAAGACGTCC SEQ ID NO:1974	-4.2	-21.3	61	-16.5	0	-8.6
1444	TGTGATCCCCACAGTTAAAG SEQ ID NO:1975	-4.2	-23.4	66.6	-17.3	-1.9	-7.8
1903	GGCATAAGTGTGATCTCTCA SEQ ID NO:1976	-4.2	-23.4	70.5	-18.7	-0.2	-6.5
2480	ATTTTTAGAAACATATTGTC SEQ ID NO:1977	-4.2	-15.6	51.8	-10.9	-0.2	-3.1
143	GAGGAACATGGTAGTTTAAG SEQ ID NO:1978	-4.1	-19.1	59.3	-15	0	-5.2
231	TCAAATCCCACACCAGCAGA SEQ ID NO:1979	-4.1	-25.7	70.2	-21.6	0	-4.1
832	GCTGTCCACACGAGAGAGAT SEQ ID NO:1980	-4.1	-25.3	71.9	-21.2	0	-3.5
846	AAAAGGCAGGTTGTGCTGTC SEQ ID NO:1981	-4.1	-23.6	69.5	-18	-1.4	-4.7
849	GGGAAAAGGCAGGTTGTGCT SEQ ID NO:1982	-4.1	-25	71.2	-18.7	-2.2	-5.2
1405	ACGAAGACCCATCAAAGTAT SEQ ID NO:1983	-4.1	-21	60.2	-16.9	0.4	-3.9
1409	AGTAACGAAGACCCATCAAA SEQ ID NO:1984	-4.1	-20.3	58.5	-15.5	-0.4	-3.3
1702	TTCTGTTGCTAGTTTCTGAA SEQ ID NO:1985	-4.1	-21.7	67.1	-17.6	0	-4.4
1739	CTCGTCCCATTATCAGAACT SEQ ID NO:1986	-4.1	-24.3	69	-20.2	0	-3
2091	AGCACAGCAAGGTGGAAAGC SEQ ID NO:1987	-4.1	-23.8	68.3	-18.8	-0.7	-5.5
2322	AGAGGTAACTTCACAAAAAT SEQ ID NO:1988	-4.1	-16.4	52.2	-11	-1.2	-4.4
2352	AAGTCCTCCACAAATTACTG SEQ ID NO:1989	-4.1	-21.3	62.3	-17.2	0	-3.2
2495	GTGAAACAAGTACCAATTTT SEQ ID NO:1990	-4.1	-18	55.3	-13.4	-0.1	-4.6
2543	ATACTCCAATTAAATGCACT SEQ ID NO:1991	-4.1	-19.2	57.7	-15.1	0	-5.5
2622	TAAATCACATCTTCTCTTAA SEQ ID NO:1992	-4.1	-17.4	55.5	-13.3	0	-2
2828	AAATTGTGCAAATATGTTAA SEQ ID NO:1993	-4.1	-15	49.3	-10.9	0	-6.1
2839	TTTGTGCTATAAAATTGTGC SEQ ID NO:1994	-4.1	-18.5	57.4	-14.4	0	-3.4
72	GCGAGTGGCTGGCGGGATCG SEQ ID NO:1995	-4	-30.3	79.7	-25.3	-0.9	-7.1
149	TCGTTCGAGGAACATGGTAG SEQ ID NO:1996	-4	-22.4	65.1	-16.5	-1.9	-6.7
222	ACACCAGCAGAATCATATCC SEQ ID NO:1997	-4	-23.4	67.2	-19.4	0	-4.1
344	AATCCATATCTTGTTGCTTG SEQ ID NO:1998	-4	-21.6	64.8	-17.6	0	-3.6
521	CTTTGCTTTCCAAAAACTTT SEQ ID NO:1999	-4	-19.6	58.6	-14.5	-1	-4.2
622	CAAGGTAGTAAAGCTGGTAT SEQ ID NO:2000	-4	-20.4	62	-16.4	0	-5.1
731	CAATCAACAGAGGGCTACCT SEQ ID NO:2001	-4	-23.8	67.6	-18.4	-1.3	-4.2

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
733	ACCAATCAACAGAGGGCTAC SEQ ID NO:2002	-4	-23.1	66.3	-19.1	0	-3.7
750	TTATGTTCACTCCGTACACC SEQ ID NO:2003	-4	-24.5	70.3	-20.5	0	-4.8
827	CCACACGAGAGAGATTGCAG SEQ ID NO:2004	-4	-23.6	67	-19.6	0	-5.2
830	TGTCCACACGAGAGAGATTG SEQ ID NO:2005	-4	-22.7	66	-18.7	0	-3.5
1424	CTCCTCTCTCCTTACAGTAA SEQ ID NO:2006	-4	-25	73.5	-21	0	-4.5
1513	AATCTCAGGACCAGCATTAA SEQ ID NO:2007	-4	-22	64.5	-18	0	-4.1
1742	AGCCTCGTCCCATTATCAGA SEQ ID NO:2008	-4	-27.7	76.9	-23.7	0	-3.2
2282	TATAACTGATATATAAATAA SEQ ID NO:2009	-4	-11.1	41.8	-7.1	0	-4.2
2451	TGAAGTGGAGGGTCCAGAAA SEQ ID NO:2010	-4	-22.8	66.1	-17.3	-1.4	-5.7
2541	ACTCCAATTAAATGCACTAC SEQ ID NO:2011	-4	-19.4	58.2	-15.4	0	-5.5
2627	CAAAATAAATCACATCTTCT SEQ ID NO:2012	-4	-15.6	50.5	-11.6	0	-1.2
2723	ACTAAGGCTAACCAAACTTA SEQ ID NO:2013	-4	-19.4	57.8	-14.7	-0.5	-3.9
2915	ATACCCAACATGTACACATC SEQ ID NO:2015	-4	-21.9	63.5	-17.9	0	-7
71	CGAGTGGCTGGCGGGATCGG SEQ ID NO:2015	-3.9	-29.7	78.1	-24.9	-0.7	-6.4
195	TCCAGTCTCTGAAGGCCTTT SEQ ID NO:2016	-3.9	-26.9	77.4	-21.5	-0.3	-10.9
370	AAGGTGTACATCAAATTCTA SEQ ID NO:2017	-3.9	-18.3	57.3	-13.9	0	-7.9
509	AAAACTTTTTCAAGTCTTTG SEQ ID NO:2018	-3.9	-16.5	53.4	-11.2	-1.3	-4.7
764	GATCAGTAGAAAGTTTATGT SEQ ID NO:2019	-3.9	-18.1	58	-14.2	0	-4.7
906	TCTATGACAGCACTTGCATC SEQ ID NO:2020	-3.9	-23.1	68.9	-18.3	-0.7	-7
947	CAACATCATCATCTTCCAGA SEQ ID NO:2021	-3.9	-22.2	65.6	-18.3	0	-2.7
1175	CCTTCAAACCACCCAAATTC SEQ ID NO:2022	-3.9	-23.6	64.4	-19.7	0	-3.1
1261	TTGACGTGTTGCTACACCAG SEQ ID NO:2023	-3.9	-24.4	69.6	-18.9	-1.6	-5.1
1393	CAAAGTATCTGCTGTCTCAC SEQ ID NO:2024	-3.9	-22	66.6	-18.1	0	-3.6
1425	GCTCCTCTCTCCTTACAGTA SEQ ID NO:2025	-3.9	-27.5	80.9	-23.6	0	-3.2
1695	GCTAGTTTCTGAATTTCGTC SEQ ID NO:2026	-3.9	-22	67.1	-18.1	0	-5
1918	AGCATTCTGACACTTGGCAT SEQ ID NO:2027	-3.9	-24.3	70.9	-19.8	-0.3	-4.1
2020	GTGGGGCACCTTGATCGTTC SEQ ID NO:2028	-3.9	-28	78.8	-22.1	-2	-10.7
2078	GGAAAGCCAGCAACTGTAAA SEQ ID NO:2029	-3.9	-21.3	61.1	-16.8	-0.3	-4.9
2093	TCAGCACAGCAAGGTGGAAA SEQ ID NO:2030	-3.9	-23.1	66.6	-18.3	-0.7	-5.5
2182	CATACAGTTTCGTACATTTT SEQ ID NO:2031	-3.9	-20	61.3	-15.6	-0.1	-4.8

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2408	GAAAATAATAGCTAGAATCT SEQ ID NO:2032	-3.9	-14.8	49.1	-10.9	0	-6.3
2824	TGTGCAAATATGTTAAGGAT SEQ ID NO:2033	-3.9	-18.1	56.2	-14.2	0	-5.4
2830	TAAAATTGTGCAAATATGTT SEQ ID NO:2034	-3.9	-15	49.3	-11.1	0	-5.6
66	GGCTGGCGGGATCGGGGGTG SEQ ID NO:2035	-3.8	-31.9	84.3	-27.2	-0.7	-6.3
224	CCACACCAGCAGAATCATAT SEQ ID NO:2036	-3.8	-23.7	66.9	-19.9	0	-4.1
253	CCAATCTTTATCATTGCCTC SEQ ID NO:2037	-3.8	-23.5	68.2	-19.2	-0.1	-3.4
467	GAATAACGATAAATTCATTA SEQ ID NO:2038	-3.8	-13.8	46.7	-9.1	-0.7	-4
841	GCAGGTTGTGCTGTCCACAC SEQ ID NO:2039	-3.8	-28.3	81.5	-22.5	-2	-7.8
1423	TCCTCTCTCCTTACAGTAAC SEQ ID NO:2040	-3.8	-24.3	72.1	-20.5	0	-4.7
1483	ACAATCTGTCTCCCGTGATA SEQ ID NO:2041	-3.8	-24.7	70.2	-20.9	0	-3.3
1572	AGGGCAAACATCACAAGGGA SEQ ID NO:2042	-3.8	-22.7	64.8	-18.9	0	-4
2356	TTCAAAGTCCTCCACAAATT SEQ ID NO:2043	-3.8	-21	61.4	-17.2	0	-2.9
2767	CTAAATTTCTTCCACCTACA SEQ ID NO:2044	-3.8	-21.6	63.2	-17.8	0	-4.9
3041	AGCTCTGTGTTGTGATTTTA SEQ ID NO:2045	-3.8	-22.3	69.2	-18.5	0	-4.3
691	CCCGGGAAAATGAACACTTT SEQ ID NO:2046	-3.7	-21.8	60.3	-17.3	0	-9.2
693	TGCCCGGGAAAATGAACACT SEQ ID NO:2047	-3.7	-23.4	63.2	-18.5	0	-10.3
776	GTATAGGAATGTGATCAGTA SEQ ID NO:2048	-3.7	-19.5	61.2	-15.8	0	-7.4
1115	TCACGACAGACTCTGGCTGC SEQ ID NO:2049	-3.7	-26.3	74.6	-21.7	-0.7	-6.8
1172	TCAAACCACCCAAATTCACA SEQ ID NO:2050	-3.7	-22.2	61.7	-18.5	0	-3.1
1227	CCACAAGCAATAAGAATCAA SEQ ID NO:2051	-3.7	-18	54.3	-14.3	0	-4.1
1403	GAAGACCCATCAAAGTATCT SEQ ID NO:2052	-3.7	-21.3	62.4	-16.9	-0.4	-3.2
1410	CAGTAACGAAGACCCATCAA SEQ ID NO:2053	-3.7	-21.7	61.4	-17.3	-0.4	-3.9
1770	GCCCCTTCAAGACAAGTAGC SEQ ID NO:2054	-3.7	-26.7	74.1	-23	0	-2.8
1803	GAGTGCATATAAGTAATTTC SEQ ID NO:2055	-3.7	-17.8	56.9	-13.6	-0.2	-6.1
2178	CAGTTTCGTACATTTTGTAT SEQ ID NO:2056	-3.7	-20.3	62.6	-15.7	-0.8	-4.8
2283	TTATAACTGATATATAAATA SEQ ID NO:2057	-3.7	-11.9	43.5	-8.2	0	-4.2
2606	TTAAAACTTGGCAAACCCTT SEQ ID NO:2058	-3.7	-20.4	58.7	-16	-0.5	-4
2612	CTTCTCTTAAAACTTGGCAA SEQ ID NO:2059	-3.7	-19.5	59	-15.8	0	-4
2734	AAGTCTGAGAAACTAAGGCT SEQ ID NO:2060	-3.7	-19.6	59.6	-15.9	0	-3.7
63	TGGCGGGATCGGGGGTGCAC SEQ ID NO:2061	-3.6	-30.7	81.5	-26	-0.7	-9.9

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
664	AAGTGCAAAAGCACCTTCCA SEQ ID NO:2062	-3.6	-23.7	66.2	-17.7	-2.4	-9
665	CAAGTGCAAAAGCACCTTCC SEQ ID NO:2063	-3.6	-23.7	66.2	-17.7	-2.4	-9
677	CACTTTTAAACACAAGTGCA SEQ ID NO:2064	-3.6	-19.2	58	-14	-1.5	-7
735	ACACCAATCAACAGAGGGCT SEQ ID NO:2065	-3.6	-24.1	68	-20.5	0	-3.7
828	TCCACACGAGAGAGATTGCA SEQ ID NO:2066	-3.6	-24	68.2	-20.4	0	-4.8
894	CTTGCATCAGAAGCAAAGTA SEQ ID NO:2067	-3.6	-20.5	61.5	-15	-1.9	-8.8
907	TTCTATGACAGCACTTGCAT SEQ ID NO:2068	-3.6	-22.8	67.7	-18.3	-0.7	-7
915	TTGGTGTGTTCTATGACAGC SEQ ID NO:2069	-3.6	-23.3	71	-19.2	-0.1	-3.9
1235	AACTTGTTCCACAAGCAATA SEQ ID NO:2070	-3.6	-20.6	60.9	-14.1	-2.9	-8.2
1482	CAATCTGTCTCCCGTGATAT SEQ ID NO:2071	-3.6	-24.5	69.6	-20.9	0	-3.3
1609	TCTTTCTTGCATGGAGATCC SEQ ID NO:2072	-3.6	-24.2	71.8	-20.6	0	-5.3
1629	CCAAGCATGATCTCTTTGCG SEQ ID NO:2073	-3.6	-24.5	69	-19.2	-1.7	-6.4
1631	ATCCAAGCATGATCTCTTTG SEQ ID NO:2074	-3.6	-22.3	66.2	-18.7	0	-4.9
1696	TGCTAGTTTCTGAATTTCGT SEQ ID NO:2075	-3.6	-21.6	65.4	-18	0	-5
1942	CTGCCGAGCAACCACTTGCT SEQ ID NO:2076	-3.6	-28.7	76	-21.7	-3.4	-9.8
2038	CTGCAAGCAGTCCACTGAGT SEQ ID NO:2077	-3.6	-26.4	75.7	-22	-0.5	-8.5
2392	ATCTTTCTGATACAGATTCC SEQ ID NO:2078	-3.6	-21.1	64.8	-16.5	-0.9	-5.9
2905	TGTACACATCCCATCTTCAA SEQ ID NO:2079	-3.6	-23.6	68.1	-20	0	-5.9
232	ATCAAATCCCACACCAGCAG SEQ ID NO:2080	-3.5	-25.1	69	-21.6	0	-4.1
259	GGCTTCCCAATCTTTATCAT SEQ ID NO:2081	-3.5	-24.7	71	-20.7	-0.1	-3.7
369	AGGTGTACATCAAATTCTAT SEQ ID NO:2082	-3.5	-19	59.3	-15	0	-7.9
1486	TCCACAATCTGTCTCCCGTG SEQ ID NO:2083	-3.5	-27.5	75.7	-24	0	-4
1544	GGCTGGTATAAGCCTTTGTA SEQ ID NO:2084	-3.5	-24.8	72.3	-18.8	-2.5	-8.7
2430	GCAACACCCAGCATTCTTTA SEQ ID NO:2085	-3.5	-25.4	71.2	-21.4	-0.1	-4.2
2653	TTTAAAAACAAAACAGAAAC SEQ ID NO:2086	-3.5	-10.2	39.9	-6.7	0	-4
2911	CCAACATGTACACATCCCAT SEQ ID NO:2087	-3.5	-24.7	68.1	-21.2	0	-7
2977	AAAGACTACAGATACAAGGA SEQ ID NO:2088	-3.5	-17.2	54	-13.7	0	-2
639	TGGATAACTCTCTCCACCAA SEQ ID NO:2089	-3.4	-23.8	67.7	-19.3	-1	-4.8
666	ACAAGTGCAAAAGCACCTTC SEQ ID NO:2090	-3.4	-21.9	63.3	-16.1	-2.4	-9
890	CATCAGAAGCAAAGTAATAC SEQ ID NO:2091	-3.4	-16.9	53.5	-13.5	0	-4.1

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
965	GTCCATCCACTACTGCTGCA SEQ ID NO:2092	-3.4	-28.5	79.8	-25.1	0	-7.1
1178	GATCCTTCAAACCACCCAAA SEQ ID NO:2093	-3.4	-24.1	65.2	-20.7	0	-3.3
1184	TTATGTGATCCTTCAAACCA SEQ ID NO:2094	-3.4	-21.6	63.2	-18.2	0	-5.5
1714	CTGATGATAAAGTTCTGTTG SEQ ID NO:2095	-3.4	-18.3	57.6	-14.9	0	-2.5
1923	TGAAGAGCATTCTGACACTT SEQ ID NO:2096	-3.4	-21.1	63.5	-16.7	-0.9	-5.2
2293	AGTGGAATAATTATAACTGA SEQ ID NO:2097	-3.4	-15.8	51.4	-12.4	0	-6.2
2323	AAGAGGTAACTTCACAAAAA SEQ ID NO:2098	-3.4	-15.7	50.5	-11	-1.2	-4.4
2611	TTCTCTTAAAACTTGGCAAA SEQ ID NO:2099	-3.4	-17.9	55.3	-14.5	0	-4
2660	AGTTTGATTTAAAAACAAAA SEQ ID NO:2100	-3.4	-11.9	43.1	-6.8	-1.7	-9.2
2724	AACTAAGGCTAACCAAACTT SEQ ID NO:2101	-3.4	-19	56.6	-14.2	-1.3	-4.2
295	TCCTTTCTTCTTAATAAGCT SEQ ID NO:2102	-3.3	-21	64	-17.7	0	-5.1
1460	AACTGCCAACTGTGTTTGTG SEQ ID NO:2103	-3.3	-23.1	67.2	-19.8	0	-3.3
1546	CTGGCTGGTATAAGCCTTTG SEQ ID NO:2104	-3.3	-24.8	71.3	-18.3	-3.2	-9.5
1863	ATCAATTTATCCACCAAAGC SEQ ID NO:2105	-3.3	-20.7	60.6	-17.4	0	-2.8
2165	TTTGTATAGATATTCCTCAC SEQ ID NO:2106	-3.3	-19.8	61.9	-16.5	0	-2.8
2333	GGGAAAATGTAAGAGGTAAC SEQ ID NO:2107	-3.3	-17.3	54.1	-14	0	-1.9
2441	GGTCCAGAAATGCAACACCC SEQ ID NO:2108	-3.3	-25.6	69.5	-21.2	-1	-5.6
2614	ATCTTCTCTTAAAACTTGGC SEQ ID NO:2109	-3.3	-19.9	61.1	-16.6	0	-2.8
2654	ATTTAAAAACAAAACAGAAA SEQ ID NO:2110	-3.3	-10	39.5	-6.7	0	-5
2959	GAAATAAAAAACACTTTTAG SEQ ID NO:2111	-3.3	-11.4	42.2	-6.9	-1.1	-3.7
2982	AAATAAAAGACTACAGATAC SEQ ID NO:2112	-3.3	-13	45.3	-9.7	0	-2.2
347	CCAAATCCATATCTTGTTGC SEQ ID NO:2113	-3.2	-22.6	65.4	-19.4	0	-2.8
563	TGGCAATTGTCTCTGTGTCT SEQ ID NO:2115	-3.2	-24.6	74	-20.9	0	-8.3
564	TTGGCAATTGTCTCTGTGTC SEQ ID NO:2115	-3.2	-23.8	72.3	-20.1	0	-8.3
591	CGATTGTCATACATATACTT SEQ ID NO:2116	-3.2	-19	58.4	-15.8	0	-4.4
701	CAACTGCTTGCCCGGGAAAA SEQ ID NO:2117	-3.2	-25.4	67	-20.6	0	-11.4
1278	GTCAGCTCCTCAAGAACTTG SEQ ID NO:2118	-3.2	-23.8	69.9	-20.6	0	-6.9
1506	GGACCAGCATTAATATGAAC SEQ ID NO:2119	-3.2	-20.1	59.7	-16.2	-0.4	-4.2
1519	CACACCAATCTCAGGACCAG SEQ ID NO:2120	-3.2	-24.9	69.7	-21.7	0	-3.7
1612	GCGTCTTTCTTGCATGGAGA SEQ ID NO:2121	-3.2	-25.6	74.2	-22.4	0	-5.1

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1616	CTTTGCGTCTTTCTTGCATG SEQ ID NO:2122	-3.2	-24.3	71.1	-20.1	-0.9	-5.1
1760	GACAAGTAGCATAATGATAG SEQ ID NO:2123	-3.2	-17.5	55.3	-14.3	0	-4.1
1838	GGCCATGTTTCAATTCACCA SEQ ID NO:2124	-3.2	-25.6	72	-22.4	0	-7
1862	TCAATTTATCCACCAAAGCC SEQ ID NO:2125	-3.2	-22.7	64.1	-19.5	0	-3.2
2171	GTACATTTTGTATAGATATT SEQ ID NO:2126	-3.2	-17.1	55.8	-13	-0.8	-4.6
2180	TACAGTTTCGTACATTTTGT SEQ ID NO:2127	-3.2	-20.5	63.2	-16.8	-0.1	-4.8
2181	ATACAGTTTCGTACATTTTG SEQ ID NO:2128	-3.2	-19.3	60	-16.1	0.7	-4.8
2391	TCTTTCTGATACAGATTCCA SEQ ID NO:2129	-3.2	-21.8	66	-17.3	-1.2	-6.2
2453	ATTGAAGTGGAGGGTCCAGA SEQ ID NO:2130	-3.2	-24.3	71	-19.2	-1.9	-6.2
2503	GAAGTATGGTGAAACAAGTA SEQ ID NO:2131	-3.2	-17.5	55	-13.3	-0.9	-3.9
734	CACCAATCAACAGAGGGCTA SEQ ID NO:2132	-3.1	-23.6	66.9	-20.5	0	-3.7
833	TGCTGTCCACACGAGAGAGA SEQ ID NO:2133	-3.1	-25.3	71.8	-22.2	0	-3.6
908	GTTCTATGACAGCACTTGCA SEQ ID NO:2134	-3.1	-24	71.1	-20	-0.7	-7
1265	GAACTTGACGTGTTGCTACA SEQ ID NO:2135	-3.1	-22.5	65.6	-18.8	-0.3	-2.4
1396	CATCAAAGTATCTGCTGTCT SEQ ID NO:2136	-3.1	-21.8	66	-18.7	0	-3.6
2058	GGGATCACGCTGAGAATGCC SEQ ID NO:2137	-3.1	-26.1	71.8	-22.5	-0.1	-5.3
2281	ATAACTGATATATAAATAAG SEQ ID NO:2138	-3.1	-11.4	42.4	-8.3	0	-4.2
2397	CTAGAATCTTTCTGATACAG SEQ ID NO:2139	-3.1	-18.5	58.5	-14.5	-0.7	-6.3
2823	GTGCAAATATGTTAAGGATT SEQ ID NO:2140	-3.1	-18.2	56.6	-15.1	0	-5.4
230	CAAATCCCACACCAGCAGAA SEQ ID NO:2141	-3	-24.6	66.7	-21.6	0	-4.1
582	TACATATACTTAACGAGCTT SEQ ID NO:2142	-3	-18.6	57.1	-15.6	0	-5.2
1109	CAGACTCTGGCTGCTCAAAT SEQ ID NO:2143	-3	-24	69.3	-21	0	-6.4
1624	CATGATCTCTTTGCGTCTTT SEQ ID NO:2144	-3	-23.4	69.5	-20.4	0	-4.9
1678	GTCATCCATGCTCAGTACTT SEQ ID NO:2145	-3	-25.3	75.2	-22.3	0	-5.7
1832	GTTTCAATTCACCAGCAAGG SEQ ID NO:2146	-3	-22.9	66.9	-19.4	-0.2	-4.7
1856	TATCCACCAAAGCCAGAGGG SEQ ID NO:2147	-3	-25.8	70.6	-22.8	0	-3.7
2330	AAAATGTAAGAGGTAACTTC SEQ ID NO:2148	-3	-15.7	51.3	-11.4	-1.2	-3.8
2752	CTACAGATAATAGACAACAA SEQ ID NO:2149	-3	-15.8	51	-12.8	0	-2
2797	CACCAATGCACTACTGTAAT SEQ ID NO:2150	-3	-21.5	62.4	-18.5	0	-5.5
2958	AAATAAAAAACACTTTTAGG SEQ ID NO:2151	-3	-12	43.3	-7.8	-1.1	-3.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
346	CAAATCCATATCTTGTTGCT SEQ ID NO:2152	-2.9	-21.5	63.6	-18.6	0	-3.6
581	ACATATACTTAACGAGCTTG SEQ ID NO:2153	-2.9	-18.9	57.6	-16	0	-6
694	TTGCCCGGGAAAATGAACAC SEQ ID NO:2154	-2.9	-22.6	61.8	-18.5	0	-10.3
729	ATCAACAGAGGGCTACCTCG SEQ ID NO:2155	-2.9	-25	70.3	-18.2	-3.9	-8.5
955	TACTGCTGCAACATCATCAT SEQ ID NO:2156	-2.9	-22.4	65.8	-19.5	0	-7.3
1427	AAGCTCCTCTCTCCTTACAG SEQ ID NO:2157	-2.9	-25.9	75.4	-23	0	-5
1441	GATCCCCACAGTTAAAGCTC SEQ ID NO:2158	-2.9	-25.3	71.2	-22.4	0	-5
1611	CGTCTTTCTTGCATGGAGAT SEQ ID NO:2159	-2.9	-23.8	69.8	-20.9	0	-5.3
1759	ACAAGTAGCATAATGATAGC SEQ ID NO:2160	-2.9	-18.7	58	-15.8	0	-4.1
1827	AATTCACCAGCAAGGATGCC SEQ ID NO:2161	-2.9	-24.8	69.2	-19.7	-2.2	-6.3
2023	TGAGTGGGGCACCTTGATCG SEQ ID NO:2162	-2.9	-26.9	74.7	-22	-2	-10.7
2179	ACAGTTTCGTACATTTTGTA SEQ ID NO:2163	-2.9	-20.5	63.2	-16.8	-0.6	-4.8
2327	ATGTAAGAGGTAACTTCACA SEQ ID NO:2164	-2.9	-19.4	60	-15.2	-1.2	-6.2
2889	TCAAATTTAAAATCATATTG SEQ ID NO:2165	-2.9	-12.4	44.3	-9.5	0	-4.7
577	ATACTTAACGAGCTTGGCAA SEQ ID NO:2166	-2.8	-21.3	62	-17.6	-0.7	-6.5
580	CATATACTTAACGAGCTTGG SEQ ID NO:2167	-2.8	-19.9	59.5	-17.1	0	-6.5
684	AAATGAACACTTTTAAACAC SEQ ID NO:2168	-2.8	-14.2	47.5	-11.4	0	-4.4
751	TTTATGTTCACTCCGTACAC SEQ ID NO:2169	-2.8	-22.6	66.9	-19.8	0	-4.8
1183	TATGTGATCCTTCAAACCAC SEQ ID NO:2170	-2.8	-21.7	63.4	-18.2	-0.5	-5.5
2039	CCTGCAAGCAGTCCACTGAG SEQ ID NO:2171	-2.8	-27.2	75.8	-23.5	-0.5	-9.3
2101	ATAGCCTCTCAGCACAGCAA SEQ ID NO:2172	-2.8	-26	74.3	-22.3	-0.7	-4.8
2325	GTAAGAGGTAACTTCACAAA SEQ ID NO:2173	-2.8	-18	56.2	-14.3	-0.7	-4.4
2474	AGAAACATATTGTCTTCTCA SEQ ID NO:2174	-2.8	-18.9	59.3	-14.5	-1.5	-5.8
2575	CAAGTATGAGCATACACTGC SEQ ID NO:2175	-2.8	-21.5	64.1	-17.2	-1.4	-9.6
106	CATGATGCCGGAGACACGGC SEQ ID NO:2176	-2.7	-27.2	72.3	-20.8	-3.7	-11.1
895	ACTTGCATCAGAAGCAAAGT SEQ ID NO:2177	-2.7	-21	62.6	-16.4	-1.9	-8.8
1217	TAAGAATCAAACGCCGGCAT SEQ ID NO:2178	-2.7	-21.9	60.5	-17.5	0	-11.6
1339	AAAGACTGGTGTGTTTCTGT SEQ ID NO:2179	-2.7	-21.8	66.5	-18.2	-0.8	-3.5
1437	CCCACAGTTAAAGCTCCTCT SEQ ID NO:2180	-2.7	-26.5	73.7	-23.8	0	-5
2017	GGGCACCTTGATCGTTCTTT SEQ ID NO:2181	-2.7	-26.7	75.6	-22.7	-1.2	-7.4

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2106	ACATCATAGCCTCTCAGCAC SEQ ID NO:2182	-2.7	-25.5	74.4	-21.9	-0.7	-4.1
2324	TAAGAGGTAACTTCACAAAA SEQ ID NO:2183	-2.7	-16.1	51.7	-12.1	-1.2	-4.4
2432	ATGCAACACCCAGCATTCTT SEQ ID NO:2184	-2.7	-25.6	71.2	-21.3	-1.6	-5.7
225	CCCACACCAGCAGAATCATA SEQ ID NO:2185	-2.6	-25.7	70.3	-23.1	0	-4.1
234	CCATCAAATCCCACACCAGC SEQ ID NO:2186	-2.6	-27.1	72	-24.5	0	-2.8
621	AAGGTAGTAAAGCTGGTATC SEQ ID NO:2187	-2.6	-20.1	62.2	-17.5	0	-5.1
669	AACACAAGTGCAAAAGCACC SEQ ID NO:2188	-2.6	-20.7	59.6	-15.7	-2.4	-9
690	CCGGGAAAATGAACACTTTT SEQ ID NO:2189	-2.6	-19.9	57.4	-17.3	0	-5.6
739	CCGTACACCAATCAACAGAG SEQ ID NO:2190	-2.6	-22.7	63.6	-20.1	0	-4.8
775	TATAGGAATGTGATCAGTAG SEQ ID NO:2191	-2.6	-18.3	58.2	-15.7	0	-7.4
914	TGGTGTGTTCTATGACAGCA SEQ ID NO:2192	-2.6	-23.9	71.8	-21.3	0.1	-5.4
1107	GACTCTGGCTGCTCAAATAT SEQ ID NO:2193	-2.6	-23	67.3	-20.4	0	-6.1
1219	AATAAGAATCAAACGCCGGC SEQ ID NO:2194	-2.6	-20.5	57.8	-16.8	0	-10.2
1267	AAGAACTTGACGTGTTGCTA SEQ ID NO:2195	-2.6	-20.9	62	-18.3	0	-5.2
1485	CCACAATCTGTCTCCCGTGA SEQ ID NO:2196	-2.6	-27.7	75.3	-25.1	0	-4.2
1919	GAGCATTCTGACACTTGGCA SEQ ID NO:2197	-2.6	-24.9	72.3	-21.7	-0.3	-4.1
2289	GAATAATTATAACTGATATA SEQ ID NO:2198	-2.6	-12.8	45.2	-10.2	0	-6.2
2372	AATATAGATTCCATTATTCA SEQ ID NO:2199	-2.6	-17.5	55.5	-14.9	0	-2.7
2545	AGATACTCCAATTAAATGCA SEQ ID NO:2200	-2.6	-18.7	56.7	-16.1	0	-5.2
2598	TGGCAAACCCTTCCCTAACT SEQ ID NO:2201	-2.6	-26.9	71.4	-23.6	-0.5	-4
2604	AAAACTTGGCAAACCCTTCC SEQ ID NO:2202	-2.6	-23	63.4	-19.7	-0.5	-4
2628	TCAAAATAAATCACATCTTC SEQ ID NO:2203	-2.6	-15.1	49.8	-12.5	0	-1.1
2818	AATATGTTAAGGATTGAGAC SEQ ID NO:2204	-2.6	-16.6	53.6	-14	0	-2.7
2832	TATAAAATTGTGCAAATATG SEQ ID NO:2205	-2.6	-13.4	46	-10.8	0	-6.1
590	GATTGTCATACATATACTTA SEQ ID NO:2206	-2.5	-17.9	57.2	-15.4	0	-3.9
692	GCCCGGGAAAATGAACACTT SEQ ID NO:2207	-2.5	-23.5	63.5	-19.8	0	-10.3
996	GCAGTTCGTTTAATTCGATG SEQ ID NO:2208	-2.5	-21.3	63.1	-18.1	-0.4	-6
1212	ATCAAACGCCGGCATCTCTG SEQ ID NO:2209	-2.5	-25.6	69.3	-21.4	0	-11.6
1223	AAGCAATAAGAATCAAACGC SEQ ID NO:2210	-2.5	-16.5	51.2	-14	0	-4.1
1387	ATCTGCTGTCTCACCTGATT SEQ ID NO:2211	-2.5	-25.4	74.7	-22.9	0	-3.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1399	ACCCATCAAAGTATCTGCTG SEQ ID NO:2212	-2.5	-23.5	67.4	-21	0	-3.6
1614	TTGCGTCTTTCTTGCATGGA SEQ ID NO:2213	-2.5	-25.1	72.8	-21.6	-0.9	-5.1
1939	CCGAGCAACCACTTGCTGAA SEQ ID NO:2215	-2.5	-25.9	69.4	-19.8	-3.6	-8.8
1943	CCTGCCGAGCAACCACTTGC SEQ ID NO:2215	-2.5	-29.8	77.4	-25	-2.3	-7.6
1946	GCCCCTGCCGAGCAACCACT SEQ ID NO:2216	-2.5	-33.7	83.4	-30.5	-0.5	-6.9
1950	GGCCGCCCCTGCCGAGCAAC SEQ ID NO:2217	-2.5	-35.7	85.9	-31.4	-1.8	-8.3
2059	AGGGATCACGCTGAGAATGC SEQ ID NO:2218	-2.5	-24.1	68.6	-21.6	0.4	-5.3
2108	CAACATCATAGCCTCTCAGC SEQ ID NO:2219	-2.5	-24.6	71.3	-22.1	0	-3.2
2128	GGCAAGATTCCGTGGGAAAT SEQ ID NO:2220	-2.5	-23.7	66	-19.7	-1.4	-6.8
2446	TGGAGGGTCCAGAAATGCAA SEQ ID NO:2221	-2.5	-23.5	66.7	-19.4	-1.5	-8.5
2542	TACTCCAATTAAATGCACTA SEQ ID NO:2222	-2.5	-18.9	57.1	-16.4	0	-5.5
2769	TCCTAAATTTCTTCCACCTA SEQ ID NO:2223	-2.5	-23.1	66.5	-20.6	0	-4.9
522	CCTTTGCTTTCCAAAAACTT SEQ ID NO:2224	-2.4	-21.5	61.8	-18	-1	-4.2
736	TACACCAATCAACAGAGGGC SEQ ID NO:2225	-2.4	-22.9	65.6	-20.5	0	-3.7
740	TCCGTACACCAATCAACAGA SEQ ID NO:2226	-2.4	-23.1	64.8	-20.7	0	-4.8
749	TATGTTCACTCCGTACACCA SEQ ID NO:2227	-2.4	-25.1	71	-22.7	0	-4.8
763	ATCAGTAGAAAGTTTATGTT SEQ ID NO:2228	-2.4	-17.6	56.9	-15.2	0	-4.6
1266	AGAACTTGACGTGTTGCTAC SEQ ID NO:2229	-2.4	-21.8	64.6	-19.4	0	-5.2
2791	TGCACTACTGTAATATTTCG SEQ ID NO:2230	-2.4	-19.7	59.8	-17.3	0	-6.8
2983	AAAATAAAAGACTACAGATA SEQ ID NO:2231	-2.4	-12.1	43.5	-9.7	0	-2.2
345	AAATCCATATCTTGTTGCTT SEQ ID NO:2232	-2.3	-20.9	62.8	-18.6	0	-3.6
368	GGTGTACATCAAATTCTATA SEQ ID NO:2233	-2.3	-18.7	58.6	-16.4	0	-7.2
730	AATCAACAGAGGGCTACCTC SEQ ID NO:2234	-2.3	-23.5	68	-18.4	-2.8	-7.2
1110	ACAGACTCTGGCTGCTCAAA SEQ ID NO:2235	-2.3	-24.2	69.9	-21	-0.7	-6.8
1185	TTTATGTGATCCTTCAAACC SEQ ID NO:2236	-2.3	-21	62.3	-18	-0.5	-5.5
1264	AACTTGACGTGTTGCTACAC SEQ ID NO:2237	-2.3	-22.1	64.8	-18.1	-1.7	-5.2
1392	AAAGTATCTGCTGTCTCACC SEQ ID NO:2238	-2.3	-23.3	69.3	-21	0	-3.6
1741	GCCTCGTCCCATTATCAGAA SEQ ID NO:2239	-2.3	-27	74.2	-24.7	0	-3
1761	AGACAAGTAGCATAATGATA SEQ ID NO:2240	-2.3	-17.5	55.3	-15.2	0	-4.1
2060	AAGGGATCACGCTGAGAATG SEQ ID NO:2241	-2.3	-21.6	62.5	-18.8	-0.1	-5.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2090	GCACAGCAAGGTGGAAAGCC SEQ ID NO:2242	-2.3	-25.8	71.6	-22.6	-0.7	-5.1
2274	ATATATAAATAAGGATTTAC SEQ ID NO:2243	-2.3	-12.6	44.9	-9.4	-0.8	-5.4
2617	CACATCTTCTCTTAAAACTT SEQ ID NO:2244	-2.3	-18.5	57.6	-16.2	0	-2.3
2758	TTCCACCTACAGATAATAGA SEQ ID NO:2245	-2.3	-20.8	61.8	-18.5	0	-2.4
199	GTACTCCAGTCTCTGAAGGC SEQ ID NO:2246	-2.2	-25.8	76.5	-23	-0.3	-4.4
223	CACACCAGCAGAATCATATC SEQ ID NO:2247	-2.2	-22.1	64.7	-19.9	0	-4.1
579	ATATACTTAACGAGCTTGGC SEQ ID NO:2248	-2.2	-21	62.3	-18.8	0	-6.5
589	ATTGTCATACATATACTTAA SEQ ID NO:2249	-2.2	-16.6	53.9	-14.4	0	-2.9
929	GAAAGATGACGCGATTGGTG SEQ ID NO:2250	-2.2	-21.1	60.5	-18.4	0	-7.9
948	GCAACATCATCATCTTCCAG SEQ ID NO:2251	-2.2	-23.4	68.5	-21.2	0	-3.4
1418	TCTCCTTACAGTAACGAAGA SEQ ID NO:2252	-2.2	-21	62.2	-18.8	0	-4.5
2284	ATTATAACTGATATATAAAT SEQ ID NO:2253	-2.2	-12.2	44	-9.4	-0.3	-4.4
2292	GTGGAATAATTATAACTGAT SEQ ID NO:2254	-2.2	-15.8	51.3	-13.6	0	-5.7
2326	TGTAAGAGGTAACTTCACAA SEQ ID NO:2255	-2.2	-18.7	58	-15.2	-1.2	-5.9
2373	CAATATAGATTCCATTATTC SEQ ID NO:2256	-2.2	-17.5	55.5	-15.3	0	-2.7
2792	ATGCACTACTGTAATATTTC SEQ ID NO:2257	-2.2	-18.9	59.2	-16.7	0	-6.8
2833	CTATAAAATTGTGCAAATAT SEQ ID NO:2258	-2.2	-14.3	47.8	-12.1	0	-6.1
58	GGATCGGGGGTGCACACACG SEQ ID NO:2259	-2.1	-28.3	75.8	-23.8	-2.4	-9.8
226	TCCCACACCAGCAGAATCAT SEQ ID NO:2260	-2.1	-26.4	72.4	-24.3	0	-4.1
752	GTTTATGTTCACTCCGTACA SEQ ID NO:2261	-2.1	-23.6	69.7	-21.5	0	-4.8
774	ATAGGAATGTGATCAGTAGA SEQ ID NO:2262	-2.1	-19.2	60.2	-17.1	0	-7.4
845	AAAGGCAGGTTGTGCTGTCC SEQ ID NO:2263	-2.1	-26.3	75.7	-22	-2.2	-6.5
1344	TCTCGAAAGACTGGTGTGTT SEQ ID NO:2264	-2.1	-22.3	66.1	-19.6	-0.3	-5.2
1547	ACTGGCTGGTATAAGCCTTT SEQ ID NO:2265	-2.1	-25	72	-19.7	-3.2	-9.5
1574	TAAGGGCAAACATCACAAGG SEQ ID NO:2266	-2.1	-19.9	58.8	-17.8	0	-3.2
1654	AATCAAATCAGGCAGCCGTT SEQ ID NO:2267	-2.1	-23.7	66.6	-20.8	-0.3	-9
2371	ATATAGATTCCATTATTCAA SEQ ID NO:2268	-2.1	-17.5	55.5	-15.4	0	-2.4
2652	TTAAAAACAAAACAGAAACA SEQ ID NO:2269	-2.1	-10.8	40.8	-8.7	0	-2
2890	TTCAAATTTAAAATCATATT SEQ ID NO:2270	-2.1	-12.5	44.5	-10.4	0	-5
113	TACCACACATGATGCCGGAG SEQ ID NO:2271	-2	-25.4	69.2	-22.9	-0.1	-6.7

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1186	CTTTATGTGATCCTTCAAAC SEQ ID NO:2272	-2	-19.9	60.5	-17.2	-0.5	-5.5
1208	AACGCCGGCATCTCTGGATC SEQ ID NO:2273	-2	-27.4	74.1	-23.8	-0.9	-11.3
1284	AACTCAGTCAGCTCCTCAAG SEQ ID NO:2274	-2	-24.2	71.4	-22.2	0	-4.4
1514	CAATCTCAGGACCAGCATTA SEQ ID NO:2275	-2	-23.4	67.8	-21.4	0	-4.1
1570	GGCAAACATCACAAGGGATA SEQ ID NO:2276	-2	-21.2	61.7	-19.2	0	-4
2164	TTGTATAGATATTCCTCACT SEQ ID NO:2277	-2	-20.6	63.6	-18.6	0	-2.8
2602	AACTTGGCAAACCCTTCCCT SEQ ID NO:2278	-2	-27.3	72.3	-25.3	0.2	-4
2796	ACCAATGCACTACTGTAATA SEQ ID NO:2279	-2	-20.5	60.7	-18.5	0	-5
2984	AAAAATAAAAGACTACAGAT SEQ ID NO:2280	-2	-11.7	42.6	-9.7	0	-2.2
3033	GTTGTGATTTTAAAGAACAA SEQ ID NO:2281	-2	-15.8	51.4	-13.1	-0.5	-7
57	GATCGGGGGTGCACACACGA SEQ ID NO:2282	-1.9	-27.7	74.6	-23.4	-2.4	-11
65	GCTGGCGGGATCGGGGGTGC SEQ ID NO:2283	-1.9	-32.5	86.1	-30.6	0	-5.7
112	ACCACACATGATGCCGGAGA SEQ ID NO:2284	-1.9	-26.3	70.9	-23.9	-0.1	-6.7
271	TTTGCAGGCATTGGCTTCCC SEQ ID NO:2285	-1.9	-28.9	80.3	-25.5	-1.3	-9.8
777	AGTATAGGAATGTGATCAGT SEQ ID NO:2286	-1.9	-19.8	62.1	-17.9	0	-7.4
997	TGCAGTTCGTTTAATTCGAT SEQ ID NO:2287	-1.9	-21.3	63.1	-18.5	-0.7	-6.3
1029	AGTGTTTGCACAGCTCGTCC SEQ ID NO:2288	-1.9	-27.5	79.4	-22.9	-2.7	-9.1
1620	ATCTCTTTGCGTCTTTCTTG SEQ ID NO:2289	-1.9	-23.5	71.1	-21.6	0	-4
1682	TTTCGTCATCCATGCTCAGT SEQ ID NO:2290	-1.9	-25.8	75.1	-23.9	0	-4.2
1887	CTCATGATGATCATGATCAC SEQ ID NO:2291	-1.9	-20.2	61.8	-14.7	-3.5	-14.2
1922	GAAGAGCATTCTGACACTTG SEQ ID NO:2292	-1.9	-21.1	63.5	-18.5	-0.4	-4.4
2657	TTGATTTAAAAACAAAACAG SEQ ID NO:2293	-1.9	-11.5	42.3	-9.6	0	-6.4
2749	CAGATAATAGACAACAAGTC SEQ ID NO:2294	-1.9	-16.6	53.2	-13.6	-1	-4.4
2802	AGACCCACCAATGCACTACT SEQ ID NO:2295	-1.9	-26.1	71.1	-24.2	0	-5.5
583	ATACATATACTTAACGAGCT SEQ ID NO:2296	-1.8	-18.5	56.8	-16.7	0	-5
1108	AGACTCTGGCTGCTCAAATA SEQ ID NO:2297	-1.8	-23	67.6	-21.2	0	-6.1
1684	AATTTCGTCATCCATGCTCA SEQ ID NO:2298	-1.8	-23.9	68.9	-22.1	0	-4.2
1688	TCTGAATTTCGTCATCCATG SEQ ID NO:2299	-1.8	-22	64.8	-20.2	0	-5
1925	GCTGAAGAGCATTCTGACAC SEQ ID NO:2300	-1.8	-22.8	67.4	-19.4	-1.6	-5.8
1954	CACAGGCCGCCCCTGCCGAG SEQ ID NO:2301	-1.8	-35.3	85.6	-30.7	-2.8	-9

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2083	AAGGTGGAAAGCCAGCAACT SEQ ID NO:2302	-1.8	-23.5	66.2	-20.2	-1.4	-6.7
2104	ATCATAGCCTCTCAGCACAG SEQ ID NO:2303	-1.8	-25.3	74.1	-22.6	-0.7	-4.1
2394	GAATCTTTCTGATACAGATT SEQ ID NO:2304	-1.8	-18.6	58.5	-15.5	-1.2	-7.6
2686	TAAAATTTTTCAGTTTTAAG SEQ ID NO:2305	-1.8	-13.6	47.3	-11.3	-0.1	-6.7
1116	TTCACGACAGACTCTGGCTG SEQ ID NO:2306	-1.7	-24.6	70.7	-22	-0.7	-6.8
1260	TGACGTGTTGCTACACCAGC SEQ ID NO:2307	-1.7	-26.1	73.4	-22.3	-2.1	-5.6
1615	TTTGCGTCTTTCTTGCATGG SEQ ID NO:2308	-1.7	-24.6	71.8	-21.9	-0.9	-5.1
2738	CAACAAGTCTGAGAAACTAA SEQ ID NO:2309	-1.7	-16.6	52.5	-14.9	0	-3
3034	TGTTGTGATTTTAAAGAACA SEQ ID NO:2310	-1.7	-16.5	53.1	-14.8	0	-4.9
56	ATCGGGGGTGCACACACGAG SEQ ID NO:2311	-1.6	-27.1	73.7	-23.1	-2.4	-11.3
294	CCTTTCTTCTTAATAAGCTG SEQ ID NO:2312	-1.6	-20.6	62.4	-19	0	-5.1
844	AAGGCAGGTTGTGCTGTCCA SEQ ID NO:2313	-1.6	-27.7	79.4	-23.5	-2.6	-7.1
1220	CAATAAGAATCAAACGCCGG SEQ ID NO:2315	-1.6	-19.4	55.5	-17.8	0	-6.2
1221	GCAATAAGAATCAAACGCCG SEQ ID NO:2315	-1.6	-20	56.7	-18.4	0	-3.4
1462	GGAACTGCCAACTGTGTTTG SEQ ID NO:2316	-1.6	-23.7	67.9	-21.6	-0.2	-3.7
2107	AACATCATAGCCTCTCAGCA SEQ ID NO:2317	-1.6	-24.6	71.3	-22.1	-0.7	-4.1
2142	ACAGTCACAGATTTGGCAAG SEQ ID NO:2318	-1.6	-21.9	65.5	-20.3	0	-4.1
2370	TATAGATTCCATTATTCAAA SEQ ID NO:2319	-1.6	-16.8	53.7	-15.2	0	-2.6
2395	AGAATCTTTCTGATACAGAT SEQ ID NO:2320	-1.6	-18.5	58.4	-15.6	-1.2	-7.3
2452	TTGAAGTGGAGGGTCCAGAA SEQ ID NO:2321	-1.6	-23.6	68.7	-20.1	-1.9	-6.2
2462	TCTTCTCAGATTGAAGTGGA SEQ ID NO:2322	-1.6	-21.4	65.8	-18.5	-1.2	-5.1
2492	AAACAAGTACCAATTTTTAG SEQ ID NO:2323	-1.6	-16	51.4	-14.4	0	-4.4
2610	TCTCTTAAAACTTGGCAAAC SEQ ID NO:2324	-1.6	-18	55.5	-16.4	0	-4
2682	ATTTTTCAGTTTTAAGTTTT SEQ ID NO:2325	-1.6	-17.5	57.4	-15.9	0	-2.6
2688	AATAAAATTTTTCAGTTTTA SEQ ID NO:2326	-1.6	-13.6	47.2	-11.3	-0.4	-6.7
2829	AAAATTGTGCAAATATGTTA SEQ ID NO:2327	-1.6	-15	49.3	-13.4	0	-6.1
2910	CAACATGTACACATCCCATC SEQ ID NO:2328	-1.6	-23.1	66.1	-21.5	0	-7
698	CTGCTTGCCCGGGAAAATGA SEQ ID NO:2329	-1.5	-25.8	68.5	-23.1	0	-10.3
904	TATGACAGCACTTGCATCAG SEQ ID NO:2330	-1.5	-22.5	66.8	-20.1	-0.7	-7.8
1176	TCCTTCAAACCACCCAAATT SEQ ID NO:2331	-1.5	-23.6	64.4	-22.1	0	-2.9

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1713	TGATGATAAAGTTCTGTTGC SEQ ID NO:2332	-1.5	-19.2	59.8	-17.7	0	-2.6
2079	TGGAAAGCCAGCAACTGTAA SEQ ID NO:2333	-1.5	-22	62.9	-19.4	-1	-6.1
2169	ACATTTTGTATAGATATTCC SEQ ID NO:2334	-1.5	-18.6	58.7	-17.1	0	-2.8
2328	AATGTAAGAGGTAACTTCAC SEQ ID NO:2335	-1.5	-18	56.8	-15.2	-1.2	-5.7
2429	CAACACCCAGCATTCTTTAA SEQ ID NO:2336	-1.5	-22.9	65.1	-21.4	0	-4.1
2635	ACAAATTTCAAAATAAATCA SEQ ID NO:2337	-1.5	-12.1	43.4	-10.6	0	-4.5
2687	ATAAAATTTTTCAGTTTTAA SEQ ID NO:2338	-1.5	-13.6	47.2	-11.3	-0.6	-6.7
700	AACTGCTTGCCCGGGAAAAT SEQ ID NO:2339	-1.4	-24.7	66	-22.1	0	-10.3
1224	CAAGCAATAAGAATCAAACG SEQ ID NO:2340	-1.4	-15.4	49	-14	0	-4.1
1428	AAAGCTCCTCTCTCCTTACA SEQ ID NO:2341	-1.4	-25.2	72.6	-23.8	0	-5
2493	GAAACAAGTACCAATTTTTA SEQ ID NO:2342	-1.4	-16.6	52.4	-15.2	0	-4.4
2544	GATACTCCAATTAAATGCAC SEQ ID NO:2343	-1.4	-18.9	57.1	-17.5	0	-5.5
349	ATCCAAATCCATATCTTGTT SEQ ID NO:2344	-1.3	-21.2	62.8	-19.9	0	-2.6
759	GTAGAAAGTTTATGTTCACT SEQ ID NO:2345	-1.3	-18.7	59.4	-16.7	-0.5	-4.6
773	TAGGAATGTGATCAGTAGAA SEQ ID NO:2346	-1.3	-18.5	58.1	-17.2	0	-7.4
1268	CAAGAACTTGACGTGTTGCT SEQ ID NO:2347	-1.3	-21.9	63.7	-20.6	0	-6.5
1461	GAACTGCCAACTGTGTTTGT SEQ ID NO:2348	-1.3	-23.7	68.6	-22.4	0	-3.5
1703	GTTCTGTTGCTAGTTTCTGA SEQ ID NO:2349	-1.3	-23.6	73.4	-22.3	0	-4.1
1945	CCCCTGCCGAGCAACCACTT SEQ ID NO:2350	-1.3	-32	79.9	-29.8	-0.7	-7.1
2601	ACTTGGCAAACCCTTCCCTA SEQ ID NO:2351	-1.3	-27.7	73.9	-25.7	-0.5	-3.2
2629	TTCAAAATAAATCACATCTT SEQ ID NO:2352	-1.3	-14.8	49	-13.5	0	-1.2
2978	AAAAGACTACAGATACAAGG SEQ ID NO:2353	-1.3	-15.9	51.1	-14.6	0	-2.2
2985	AAAAAATAAAAGACTACAGA SEQ ID NO:2354	-1.3	-11	41.3	-9.7	0	-2.2
2996	AGCAGTCATTTAAAAAATAA SEQ ID NO:2355	-1.3	-14.2	47.7	-12.9	0	-5
3032	TTGTGATTTTAAAGAACAAG SEQ ID NO:2356	-1.3	-14.6	48.8	-12.8	-0.2	-6.4
3038	TCTGTGTTGTGATTTTAAAG SEQ ID NO:2357	-1.3	-18.2	58	-16.9	0	-4.6
741	CTCCGTACACCAATCAACAG SEQ ID NO:2358	-1.2	-23.4	65.3	-22.2	0	-4.8
928	AAAGATGACGCGATTGGTGT SEQ ID NO:2359	-1.2	-21.7	62.1	-19.8	-0.5	-7.9
951	GCTGCAACATCATCATCTTC SEQ ID NO:2360	-1.2	-23.4	69.4	-22.2	0	-5.8
982	TCGATGGATAGAAAGACGTC SEQ ID NO:2361	-1.2	-19.7	58.7	-18	0	-8.2

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1024	TTGCACAGCTCGTCCGGGGT SEQ ID NO:2362	-1.2	-30.6	82.6	-28.8	-0.3	-6.9
1179	TGATCCTTCAAACCACCCAA SEQ ID NO:2363	-1.2	-24.8	67.1	-23.1	-0.1	-4.3
2037	TGCAAGCAGTCCACTGAGTG SEQ ID NO:2364	-1.2	-25.5	73.5	-23.1	-1.1	-6.9
2396	TAGAATCTTTCTGATACAGA SEQ ID NO:2365	-1.2	-18.2	57.8	-15.9	-1	-6.1
2605	TAAAACTTGGCAAACCCTTC SEQ ID NO:2366	-1.2	-20.7	59.6	-18.8	-0.5	-4
2683	AATTTTTCAGTTTTAAGTTT SEQ ID NO:2367	-1.2	-16.7	55	-15.5	0	-2.6
2748	AGATAATAGACAACAAGTCT SEQ ID NO:2368	-1.2	-16.8	53.8	-13.8	-1.8	-5.7
3005	ATGTCATTCAGCAGTCATTT SEQ ID NO:2369	-1.2	-22.5	69.3	-21.3	0	-4.1
55	TCGGGGGTGCACACACGAGC SEQ ID NO:2370	-1.1	-28.9	77.8	-25.4	-2.4	-10.6
748	ATGTTCACTCCGTACACCAA SEQ ID NO:2371	-1.1	-24.7	69.3	-23.6	0	-4.8
1400	GACCCATCAAAGTATCTGCT SEQ ID NO:2372	-1.1	-24.1	68.8	-23	0	-3.6
1463	TGGAACTGCCAACTGTGTTT SEQ ID NO:2373	-1.1	-23.7	67.9	-21.6	-0.9	-5.4
1610	GTCTTTCTTGCATGGAGATC SEQ ID NO:2374	-1.1	-23.4	71.5	-22.3	0	-5.1
2057	GGATCACGCTGAGAATGCCC SEQ ID NO:2375	-1.1	-26.9	72.8	-25.3	-0.1	-5.3
2369	ATAGATTCCATTATTCAAAG SEQ ID NO:2376	-1.1	-17.1	54.4	-16	0	-2.6
2440	GTCCAGAAATGCAACACCCA SEQ ID NO:2377	-1.1	-25.1	68.2	-23.3	-0.4	-5.6
2494	TGAAACAAGTACCAATTTTT SEQ ID NO:2378	-1.1	-16.9	52.9	-15.8	0	-4.4
2737	AACAAGTCTGAGAAACTAAG SEQ ID NO:2379	-1.1	-15.9	51.4	-14.8	0	-3
2834	GCTATAAAATTGTGCAAATA SEQ ID NO:2380	-1.1	-16.1	51.3	-15	0	-6.1
198	TACTCCAGTCTCTGAAGGCC SEQ ID NO:2381	-1	-26.6	76.6	-25.1	-0.1	-6.3
903	ATGACAGCACTTGCATCAGA SEQ ID NO:2382	-1	-23.4	68.7	-21.5	-0.7	-7.8
927	AAGATGACGCGATTGGTGTG SEQ ID NO:2383	-1	-22.4	64	-20.5	-0.7	-7.9
1211	TCAAACGCCGGCATCTCTGG SEQ ID NO:2384	-1	-26.8	71.7	-24.1	-0.5	-11.6
1628	CAAGCATGATCTCTTTGCGT SEQ ID NO:2385	-1	-23.7	68.6	-21	-1.7	-6.4
1837	GCCATGTTTCAATTCACCAG SEQ ID NO:2386	-1	-24.4	69.8	-23.4	0	-4.3
2028	TCCACTGAGTGGGGCACCTT SEQ ID NO:2387	-1	-29.3	81	-26	-2.3	-10.6
2055	ATCACGCTGAGAATGCCCTG SEQ ID NO:2388	-1	-26	70.9	-24.5	-0.1	-5.1
2126	CAAGATTCCGTGGGAAATCA SEQ ID NO:2389	-1	-21.8	62.3	-18.9	-1.9	-7.1
2321	GAGGTAACTTCACAAAAATC SEQ ID NO:2390	-1	-16.8	53.2	-14.5	-1.2	-4.4
2412	TAAAGAAAATAATAGCTAGA SEQ ID NO:2391	-1	-12.5	44.4	-11.5	0	-6.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2751	TACAGATAATAGACAACAAG SEQ ID NO:2392	-1	-14.9	49.3	-13.9	0	-1.2
2757	TCCACCTACAGATAATAGAC SEQ ID NO:2393	-1	-20.9	62	-19.9	0	-2.3
2794	CAATGCACTACTGTAATATT SEQ ID NO:2394	-1	-18.4	56.8	-17.4	0	-5.5
114	ATACCACACATGATGCCGGA SEQ ID NO:2395	-0.9	-25.4	68.9	-24	-0.1	-6.7
233	CATCAAATCCCACACCAGCA SEQ ID NO:2396	-0.9	-25.8	69.8	-24.9	0	-4.1
288	TTCTTAATAAGCTGGGTTTT SEQ ID NO:2397	-0.9	-20.1	61.9	-19.2	0	-5.1
523	GCCTTTGCTTTCCAAAAACT SEQ ID NO:2398	-0.9	-23.2	65.2	-21.2	-1	-5.4
910	GTGTTCTATGACAGCACTTG SEQ ID NO:2399	-0.9	-22.7	68.7	-21.1	-0.5	-5.3
1248	ACACCAGCATGGTAACTTGT SEQ ID NO:2400	-0.9	-24.1	69.4	-20.5	-2.7	-8.2
1625	GCATGATCTCTTTGCGTCTT SEQ ID NO:2401	-0.9	-25.1	73.6	-23.2	-0.9	-5.7
1846	AGCCAGAGGGCCATGTTTCA SEQ ID NO:2402	-0.9	-28.5	80	-24.9	-2.7	-9.5
2428	AACACCCAGCATTCTTTAAA SEQ ID NO:2403	-0.9	-21.5	62	-20.6	0	-4.1
2638	GAAACAAATTTCAAAATAAA SEQ ID NO:2404	-0.9	-10.2	39.9	-7.7	-1.6	-5.6
2735	CAAGTCTGAGAAACTAAGGC SEQ ID NO:2405	-0.9	-19.4	59	-18.5	0	-3
2750	ACAGATAATAGACAACAAGT SEQ ID NO:2406	-0.9	-16.4	52.5	-15.5	0	-2.9
46	CACACACGAGCTTCGGTGGG SEQ ID NO:2407	-0.8	-26.9	73.5	-22.9	-3.2	-10.9
74	GGGCGAGTGGCTGGCGGGAT SEQ ID NO:2408	-0.8	-31.5	83.4	-29	-1.7	-6.3
227	ATCCCACACCAGCAGAATCA SEQ ID NO:2409	-0.8	-26.4	72.4	-25.6	0	-4.1
949	TGCAACATCATCATCTTCCA SEQ ID NO:2410	-0.8	-23.4	68.1	-22.6	0	-4.7
1573	AAGGGCAAACATCACAAGGG SEQ ID NO:2411	-0.8	-21.4	61.6	-20.6	0	-4
1655	TAATCAAATCAGGCAGCCGT SEQ ID NO:2412	-0.8	-23.3	65.7	-21.7	-0.3	-9
2409	AGAAAATAATAGCTAGAATC SEQ ID NO:2413	-0.8	-13.9	47.4	-13.1	0	-6.3
2463	GTCTTCTCAGATTGAAGTGG SEQ ID NO:2415	-0.8	-22	67.8	-19.9	-1.2	-5.9
348	TCCAAATCCATATCTTGTTG SEQ ID NO:2415	-0.7	-21.2	62.8	-20.5	0	-2.7
510	AAAAACTTTTTCAAGTCTTT SEQ ID NO:2416	-0.7	-15.8	51.7	-13.7	-1.3	-4.7
1114	CACGACAGACTCTGGCTGCT SEQ ID NO:2417	-0.7	-26.8	74.8	-26.1	0.2	-6.4
1273	CTCCTCAAGAACTTGACGTG SEQ ID NO:2418	-0.7	-22.5	64.7	-20.8	-0.8	-8.9
1548	AACTGGCTGGTATAAGCCTT SEQ ID NO:2419	-0.7	-24.2	69.3	-20.3	-3.2	-9.5
1552	TACAAACTGGCTGGTATAAG SEQ ID NO:2420	-0.7	-19.3	58.5	-18.6	0	-5
2081	GGTGGAAAGCCAGCAACTGT SEQ ID NO:2421	-0.7	-25.4	71	-24.7	3.2	-6.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2098	GCCTCTCAGCACAGCAAGGT SEQ ID NO:2422	-0.7	-28.7	81.2	-27.1	-0.7	-5.1
2390	CTTTCTGATACAGATTCCAA SEQ ID NO:2423	-0.7	-20.7	62.3	-18.7	-1.2	-6.2
2812	TTAAGGATTGAGACCCACCA SEQ ID NO:2424	-0.7	-24	67.1	-22.8	-0.2	-3.7
2891	CTTCAAATTTAAAATCATAT SEQ ID NO:2425	-0.7	-13.3	46	-12.6	0	-5
2909	AACATGTACACATCCCATCT SEQ ID NO:2426	-0.7	-23.3	66.8	-22.6	0	-7
3006	TATGTCATTCAGCAGTCATT SEQ ID NO:2427	-0.7	-22.1	68.2	-21.4	0	-4.1
229	AAATCCCACACCAGCAGAAT SEQ ID NO:2428	-0.6	-23.9	65.7	-23.3	0	-4.1
578	TATACTTAACGAGCTTGGCA SEQ ID NO:2429	-0.6	-21.7	63.5	-20.2	-0.7	-6.5
758	TAGAAAGTTTATGTTCACTC SEQ ID NO:2430	-0.6	-17.9	57.6	-16.6	-0.5	-4.6
939	TCATCTTCCAGAAAGATGAC SEQ ID NO:2431	-0.6	-20.2	61.2	-15.1	-4.5	-10.5
2170	TACATTTTGTATAGATATTC SEQ ID NO:2432	-0.6	-16.3	54.1	-15.1	-0.3	-3.4
2285	AATTATAACTGATATATAAA SEQ ID NO:2433	-0.6	-11.5	42.6	-10.3	-0.3	-4.4
2320	AGGTAACTTCACAAAAATCA SEQ ID NO:2434	-0.6	-16.9	53.2	-15.4	-0.7	-3.3
2393	AATCTTTCTGATACAGATTC SEQ ID NO:2435	-0.6	-18.4	58.6	-16.5	-1.2	-7.2
2411	AAAGAAAATAATAGCTAGAA SEQ ID NO:2436	-0.6	-12.1	43.5	-11.5	0	-6.3
2414	TTTAAAGAAAATAATAGCTA SEQ ID NO:2437	-0.6	-12.1	43.7	-11.5	0	-6
2636	AACAAATTTCAAAATAAATC SEQ ID NO:2438	-0.6	-10.7	40.9	-10.1	0	-4.5
2900	ACATCCCATCTTCAAATTTA SEQ ID NO:2439	-0.6	-21	62	-20.4	0	-4.7
3039	CTCTGTGTTGTGATTTTAAA SEQ ID NO:2440	-0.6	-19.1	59.8	-18.5	0	-4.2
75	GGGGCGAGTGGCTGGCGGGA SEQ ID NO:2441	-0.5	-32.7	86	-30.5	-1.7	-6.3
792	TTGCCTGTTCTGTAGAGTAT SEQ ID NO:2442	-0.5	-23.8	72.2	-23.3	0	-3.2
964	TCCATCCACTACTGCTGCAA SEQ ID NO:2443	-0.5	-26.6	73.8	-26.1	0	-7.3
983	TTCGATGGATAGAAAGACGT SEQ ID NO:2444	-0.5	-19.4	57.8	-18.9	0	-5.2
1225	ACAAGCAATAAGAATCAAAC SEQ ID NO:2445	-0.5	-14.8	48.5	-14.3	0	-4.1
1226	CACAAGCAATAAGAATCAAA SEQ ID NO:2446	-0.5	-15.3	49.2	-14.8	0	-3.3
2054	TCACGCTGAGAATGCCCTGC SEQ ID NO:2447	-0.5	-27.8	74.9	-27.3	0	-4.2
2275	GATATATAAATAAGGATTTA SEQ ID NO:2448	-0.5	-13	45.7	-11.3	-1.1	-5.6
2413	TTAAAGAAAATAATAGCTAG SEQ ID NO:2449	-0.5	-12	43.5	-11.5	0	-6.3
2634	CAAATTTCAAAATAAATCAC SEQ ID NO:2450	-0.5	-12.1	43.4	-11.6	0	-4.5
2656	TGATTTAAAAACAAAACAGA SEQ ID NO:2451	-0.5	-12	43.1	-11.5	0	-5

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2736	ACAAGTCTGAGAAACTAAGG SEQ ID NO:2452	-0.5	-17.8	55.6	-17.3	0	-3
2773	CGCTTCCTAAATTTCTTCCA SEQ ID NO:2453	-0.5	-23.9	67.5	-23.4	0	-4.9
111	CCACACATGATGCCGGAGAC SEQ ID NO:2454	-0.4	-26.3	70.9	-25.9	0	-6.7
995	CAGTTCGTTTAATTCGATGG SEQ ID NO:2455	-0.4	-20.7	61.6	-19.4	-0.7	-6.3
1415	CCTTACAGTAACGAAGACCC SEQ ID NO:2456	-0.4	-23.5	65.2	-23.1	0	-4.7
1683	ATTTCGTCATCCATGCTCAG SEQ ID NO:2457	-0.4	-24.6	71.5	-24.2	0	-4.2
2084	CAAGGTGGAAAGCCAGCAAC SEQ ID NO:2458	-0.4	-23.3	65.5	-21.5	-1.3	-6.7
2280	TAACTGATATATAAATAAGG SEQ ID NO:2459	-0.4	-12.6	44.7	-12.2	0	-4.2
2690	CCAATAAAATTTTTCAGTTT SEQ ID NO:2460	-0.4	-16.5	52.5	-16.1	0	-6.4
2739	ACAACAAGTCTGAGAAACTA SEQ ID NO:2461	-0.4	-17.5	54.7	-17.1	0	-3
2756	CCACCTACAGATAATAGACA SEQ ID NO:2462	-0.4	-21.2	61.8	-20.8	0	-2.4
3007	ATATGTCATTCAGCAGTCAT SEQ ID NO:2463	-0.4	-22	67.8	-21.6	0	-4.1
270	TTGCAGGCATTGGCTTCCCA SEQ ID NO:2464	-0.3	-29.5	81	-27.7	-1.3	-9.8
286	CTTAATAAGCTGGGTTTTGC SEQ ID NO:2465	-0.3	-21.4	64.2	-21.1	0	-5.1
1685	GAATTTCGTCATCCATGCTC SEQ ID NO:2466	-0.3	-23.8	69.1	-23.5	0	-4.4
2651	TAAAAACAAAACAGAAACAA SEQ ID NO:2467	-0.3	-10	39.4	-9.7	0	0
2793	AATGCACTACTGTAATATTT SEQ ID NO:2468	-0.3	-17.8	55.9	-17.5	0	-6.8
2803	GAGACCCACCAATGCACTAC SEQ ID NO:2469	-0.3	-25.8	70.5	-25.5	0	-5.5
365	GTACATCAAATTCTATATCC SEQ ID NO:2470	-0.2	-18.7	58.2	-18.5	0	-4.6
1111	GACAGACTCTGGCTGCTCAA SEQ ID NO:2471	-0.2	-25.5	73.6	-24.4	-0.7	-6.8
1177	ATCCTTCAAACCACCCAAAT SEQ ID NO:2472	-0.2	-23.5	64.1	-23.3	0	-1
1277	TCAGCTCCTCAAGAACTTGA SEQ ID NO:2473	-0.2	-23.2	67.9	-22.1	-0.6	-8.7
1416	TCCTTACAGTAACGAAGACC SEQ ID NO:2474	-0.2	-21.9	63.1	-21.7	0	-4.7
2082	AGGTGGAAAGCCAGCAACTG SEQ ID NO:2475	-0.2	-24.2	68.2	-22.5	-1.4	-6.7
2100	TAGCCTCTCAGCACAGCAAG SEQ ID NO:2476	-0.2	-26	74.7	-24.9	-0.7	-4.8
2630	TTTCAAAATAAATCACATCT SEQ ID NO:2477	-0.2	-14.8	49	-14.6	0	-1.7
2747	GATAATAGACAACAAGTCTG SEQ ID NO:2478	-0.2	-16.8	53.6	-14.6	-2	-5.7
2899	CATCCCATCTTCAAATTTAA SEQ ID NO:2479	-0.2	-20.1	59.5	-19.9	0	-4.7
525	TAGCCTTTGCTTTCCAAAAA SEQ ID NO:2480	-0.1	-21.8	62.6	-20.3	-1.3	-5.9
678	ACACTTTTAAACACAAGTGC SEQ ID NO:2481	-0.1	-18.7	57.3	-16.2	-2.4	-8.7

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
940	ATCATCTTCCAGAAAGATGA SEQ ID NO:2482	-0.1	-20	60.6	-15.1	-4.8	-11.1
1210	CAAACGCCGGCATCTCTGGA SEQ ID NO:2483	-0.1	-27	71.4	-25.3	-0.9	-11.1
1391	AAGTATCTGCTGTCTCACCT SEQ ID NO:2484	-0.1	-24.9	73.8	-24.8	0	-3.6
1963	ACAAATTACCACAGGCCGCC SEQ ID NO:2485	-0.1	-26.7	70.4	-26.1	0	-7.7
2029	GTCCACTGAGTGGGGCACCT SEQ ID NO:2486	-0.1	-30.4	84.3	-28	-2.3	-10.6
2332	GGAAAATGTAAGAGGTAACT SEQ ID NO:2487	-0.1	-17	53.5	-15.8	-1	-3.5
2691	ACCAATAAAATTTTTCAGTT SEQ ID NO:2488	-0.1	-16.6	52.7	-16.5	0	-6.7
2693	CTACCAATAAAATTTTTCAG SEQ ID NO:2489	-0.1	-15.9	51	-15.8	0	-6.7
2771	CTTCCTAAATTTCTTCCACC SEQ ID NO:2490	-0.1	-23.5	67.4	-23.4	0	-4.9
3031	TGTGATTTTAAAGAACAAGA SEQ ID NO:2491	-0.1	-15.1	49.8	-15	0	-4.6
287	TCTTAATAAGCTGGGTTTTG SEQ ID NO:2492	0	-20	61.5	-20	0	-5.1
367	GTGTACATCAAATTCTATAT SEQ ID NO:2493	0	-17.5	55.9	-17.5	0	-6.6
742	ACTCCGTACACCAATCAACA SEQ ID NO:2494	0	-23.6	65.6	-23.6	0	-4.3
772	AGGAATGTGATCAGTAGAAA SEQ ID NO:2495	0	-18.1	56.7	-18.1	0	-6.6
848	GGAAAAGGCAGGTTGTGCTG SEQ ID NO:2496	0	-23.8	68.5	-21.6	-2.2	-5.2
909	TGTTCTATGACAGCACTTGC SEQ ID NO:2497	0	-23.3	69.7	-23.3	0	-5.7
1247	CACCAGCATGGTAACTTGTT SEQ ID NO:2498	0	-24	69.2	-21.3	-2.7	-9
1272	TCCTCAAGAACTTGACGTGT SEQ ID NO:2499	0	-22.8	65.9	-21.8	-0.8	-8.9
1962	CAAATTACCACAGGCCGCCC SEQ ID NO:2500	0	-28.5	73	-28	0	-7.7
2418	ATTCTTTAAAGAAAATAATA SEQ ID NO:2501	0	-11.1	41.8	-9.1	-0.9	-12.2
2427	ACACCCAGCATTCTTTAAAG SEQ ID NO:2502	0	-22.2	64.2	-22.2	0	-7.4
2433	AATGCAACACCCAGCATTCT SEQ ID NO:2503	0	-24.8	68.7	-22.2	-2.6	-7.6
2684	AAATTTTTCAGTTTTAAGTT SEQ ID NO:2504	0	-15.9	52.7	-15.9	0	-4.3
2692	TACCAATAAAATTTTTCAGT SEQ ID NO:2505	0	-16.2	51.9	-16.2	0	-6.7
2709	AACTTAGATATAAATCCTAC SEQ ID NO:2506	0	-16	51.8	-15.1	-0.7	-4.2
2995	GCAGTCATTTAAAAAATAAA SEQ ID NO:2507	0	-13.5	46.1	-12.9	-0.3	-5
524	AGCCTTTGCTTTCCAAAAAC SEQ ID NO:2508	0.1	-22.3	63.6	-21.2	-1.1	-5.9
1845	GCCAGAGGGCCATGTTTCAA SEQ ID NO:2509	0.1	-27.8	77.1	-26	-1.9	-9.5
2040	CCCTGCAAGCAGTCCACTGA SEQ ID NO:2510	0.1	-29.2	79	-28.4	-0.5	-9.3
2099	AGCCTCTCAGCACAGCAAGG SEQ ID NO:2511	0.1	-27.5	77.9	-26.7	-0.7	-4.9

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2109	TCAACATCATAGCCTCTCAG SEQ ID NO:2512	0.1	-23.2	68.6	-23.3	0	-3.2
2119	CCGTGGGAAATCAACATCAT SEQ ID NO:2513	0.1	-22	62.2	-21.6	-0.2	-4.2
2609	CTCTTAAAACTTGGCAAACC SEQ ID NO:2515	0.1	-19.6	57.9	-19.2	-0.1	-4
2699	TAAATCCTACCAATAAAATT SEQ ID NO:2515	0.1	-15.2	48.9	-15.3	0	-2.9
2722	CTAAGGCTAACCAAACTTAG SEQ ID NO:2516	0.1	-19.2	57.5	-17.9	-1.3	-5.8
697	TGCTTGCCCGGGAAAATGAA SEQ ID NO:2517	0.2	-24.2	64.9	-23.2	0	-10.3
1388	TATCTGCTGTCTCACCTGAT SEQ ID NO:2518	0.2	-25	73.7	-25.2	0	-3
2036	GCAAGCAGTCCACTGAGTGG SEQ ID NO:2519	0.2	-26.7	76.4	-25	-1.9	-8.9
2163	TGTATAGATATTCCTCACTC SEQ ID NO:2520	0.2	-20.9	64.8	-21.1	0	-2.8
2287	ATAATTATAACTGATATATA SEQ ID NO:2521	0.2	-12.6	45	-12.8	0	-5.3
2645	CAAAACAGAAACAAATTTCA SEQ ID NO:2522	0.2	-13.5	45.8	-11.3	-2.4	-5.5
2813	GTTAAGGATTGAGACCCACC SEQ ID NO:2523	0.2	-24.5	69.1	-24.7	0.6	-2.9
2992	GTCATTTAAAAAATAAAAGA SEQ ID NO:2524	0.2	-10.9	41.3	-10.3	-0.6	-5
42	CACGAGCTTCGGTGGGCAAT SEQ ID NO:2525	0.3	-26.9	73	-25.7	-1.4	-7.3
236	CTCCATCAAATCCCACACCA SEQ ID NO:2526	0.3	-26.6	71.1	-26.9	0	-1.1
687	GGAAAATGAACACTTTTAAA SEQ ID NO:2527	0.3	-14.2	47.3	-14.5	0	-4.4
688	GGGAAAATGAACACTTTTAA SEQ ID NO:2528	0.3	-16.1	51.1	-16.4	0	-4.4
1112	CGACAGACTCTGGCTGCTCA SEQ ID NO:2529	0.3	-27	75.9	-26.4	-0.8	-6.8
1242	GCATGGTAACTTGTTCCACA SEQ ID NO:2530	0.3	-24.4	70.5	-23.1	-1.5	-7.2
1274	GCTCCTCAAGAACTTGACGT SEQ ID NO:2531	0.3	-24.3	68.9	-23.7	-0.6	-8.7
2041	GCCCTGCAAGCAGTCCACTG SEQ ID NO:2532	0.3	-30.4	81.9	-29.8	-0.2	-9.3
2286	TAATTATAACTGATATATAA SEQ ID NO:2533	0.3	-11.9	43.5	-11.7	-0.1	-4.4
2329	AAATGTAAGAGGTAACTTCA SEQ ID NO:2534	0.3	-17.1	54.4	-16.1	-1.2	-5.6
2700	ATAAATCCTACCAATAAAAT SEQ ID NO:2535	0.3	-15.1	48.6	-15.4	0	-1.2
2768	CCTAAATTTCTTCCACCTAC SEQ ID NO:2536	0.3	-22.9	65.6	-23.2	0	-4.9
289	CTTCTTAATAAGCTGGGTTT SEQ ID NO:2537	0.4	-20.9	63.5	-21.3	0	-5.1
350	TATCCAAATCCATATCTTGT SEQ ID NO:2538	0.4	-20.8	61.9	-21.2	0	-2.6
791	TGCCTGTTCTGTAGAGTATA SEQ ID NO:2539	0.4	-23.4	71.2	-23.8	0	-3.2
793	TTTGCCTGTTCTGTAGAGTA SEQ ID NO:2540	0.4	-23.9	72.7	-24.3	0	-3.2
843	AGGCAGGTTGTGCTGTCCAC SEQ ID NO:2541	0.4	-28.6	82.9	-26.4	-2.6	-7.1

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1402	AAGACCCATCAAAGTATCTG SEQ ID NO:2542	0.4	-20.7	61	-20.4	-0.4	-3.3
2376	TTCCAATATAGATTCCATTA SEQ ID NO:2543	0.4	-19.5	59.4	-19.9	0	-2.4
2377	ATTCCAATATAGATTCCATT SEQ ID NO:2544	0.4	-19.8	59.9	-20.2	0	-2.7
2450	GAAGTGGAGGGTCCAGAAAT SEQ ID NO:2545	0.4	-22.8	66.2	-21.3	-1.9	-6.2
2465	TTGTCTTCTCAGATTGAAGT SEQ ID NO:2546	0.4	-20.9	65.4	-20	-1.2	-5.9
2616	ACATCTTCTCTTAAAACTTG SEQ ID NO:2547	0.4	-17.8	56.3	-18.2	0	-2.3
2901	CACATCCCATCTTCAAATTT SEQ ID NO:2548	0.4	-22	63.7	-22.4	0	-4.3
228	AATCCCACACCAGCAGAATC SEQ ID NO:2549	0.5	-25	69.1	-25.5	0	-4.1
757	AGAAAGTTTATGTTCACTCC SEQ ID NO:2550	0.5	-20.2	62.2	-20	-0.5	-4.6
1484	CACAATCTGTCTCCCGTGAT SEQ ID NO:2551	0.5	-25.7	71.8	-26.2	0	-3.9
1677	TCATCCATGCTCAGTACTTC SEQ ID NO:2552	0.5	-24.5	73.3	-25	0	-5.7
1847	AAGCCAGAGGGCCATGTTTC SEQ ID NO:2553	0.5	-27.1	76.3	-24.9	-2.7	-9.5
2143	TACAGTCACAGATTTGGCAA SEQ ID NO:2554	0.5	-21.6	64.7	-22.1	0	-4.1
2148	CACTCTACAGTCACAGATTT SEQ ID NO:2555	0.5	-21.7	66.2	-22.2	0	-2.8
2374	CCAATATAGATTCCATTATT SEQ ID NO:2556	0.5	-19.1	58	-19.6	0	-2.7
2466	ATTGTCTTCTCAGATTGAAG SEQ ID NO:2557	0.5	-19.7	62	-19.6	-0.3	-5.6
2795	CCAATGCACTACTGTAATAT SEQ ID NO:2558	0.5	-20.3	60.2	-20.8	0	-5.5
3008	AATATGTCATTCAGCAGTCA SEQ ID NO:2559	0.5	-21.3	65.4	-21.8	0	-4.1
911	TGTGTTCTATGACAGCACTT SEQ ID NO:2560	0.6	-22.7	68.7	-22	-1.2	-5.2
1613	TGCGTCTTTCTTGCATGGAG SEQ ID NO:2561	0.6	-25	72.7	-24.7	-0.7	-5.1
1626	AGCATGATCTCTTTGCGTCT SEQ ID NO:2562	0.6	-25	73.5	-23.9	-1.7	-6.4
1686	TGAATTTCGTCATCCATGCT SEQ ID NO:2563	0.6	-23.4	67.4	-24	0	-5
1828	CAATTCACCAGCAAGGATGC SEQ ID NO:2564	0.6	-23.5	66.8	-22.3	-1.8	-6.1
1841	GAGGGCCATGTTTCAATTCA SEQ ID NO:2565	0.6	-24.5	70.9	-24.6	0	-7.6
2144	CTACAGTCACAGATTTGGCA SEQ ID NO:2566	0.6	-23.2	68.9	-23.8	0	-4
2997	CAGCAGTCATTTAAAAAATA SEQ ID NO:2567	0.6	-15.6	50.5	-16.2	0	-5
1855	ATCCACCAAAGCCAGAGGGC SEQ ID NO:2568	0.7	-27.9	75.1	-26.3	-2.3	-6.2
1944	CCCTGCCGAGCAACCACTTG SEQ ID NO:2569	0.7	-30	76.7	-29.8	-0.7	-7.1
2032	GCAGTCCACTGAGTGGGGCA SEQ ID NO:2570	0.7	-29.8	84.1	-28.1	-2.4	-10.6
2118	CGTGGGAAATCAACATCATA SEQ ID NO:2571	0.7	-19.7	58.2	-19.9	-0.2	-2.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2375	TCCAATATAGATTCCATTAT SEQ ID NO:2572	0.7	-19.4	59	-20.1	0	-2.7
2633	AAATTTCAAAATAAATCACA SEQ ID NO:2573	0.7	-12.1	43.4	-12.8	0	-4.3
2702	ATATAAATCCTACCAATAAA SEQ ID NO:2574	0.7	-15.5	49.6	-16.2	0	-2.5
2898	ATCCCATCTTCAAATTTAAA SEQ ID NO:2575	0.7	-18.7	56.5	-19.4	0	-4.7
3019	GAACAAGATAAAATATGTCA SEQ ID NO:2576	0.7	-14.3	47.8	-15	0	-3.5
272	TTTTGCAGGCATTGGCTTCC SEQ ID NO:2577	0.8	-27	77.1	-26.3	-1.3	-9.8
354	TCTATATCCAAATCCATATC SEQ ID NO:2578	0.8	-19.6	59.5	-20.4	0	-2.4
680	GAACACTTTTAAACACAAGT SEQ ID NO:2579	0.8	-16.8	53	-17.6	0	-4.4
689	CGGGAAAATGAACACTTTTA SEQ ID NO:2580	0.8	-17.6	53.5	-18.4	0	-4.4
842	GGCAGGTTGTGCTGTCCACA SEQ ID NO:2581	0.8	-29.3	83.6	-27.9	-2.2	-7.6
1436	CCACAGTTAAAGCTCCTCTC SEQ ID NO:2582	0.8	-24.9	71.8	-25.7	0	-5
1473	TCCCGTGATATGGAACTGCC SEQ ID NO:2583	0.8	-26.7	72.1	-27	-0.2	-3.4
1569	GCAAACATCACAAGGGATAC SEQ ID NO:2584	0.8	-20.2	59.8	-21	0	-3.5
1676	CATCCATGCTCAGTACTTCC SEQ ID NO:2585	0.8	-26.1	75.3	-26.9	0	-5.7
1740	CCTCGTCCCATTATCAGAAC SEQ ID NO:2586	0.8	-25.4	70.6	-26.2	0	-3
2380	CAGATTCCAATATAGATTCC SEQ ID NO:2587	0.8	-20.3	61.1	-21.1	0	-2.7
2701	TATAAATCCTACCAATAAAA SEQ ID NO:2588	0.8	-14.8	48.1	-15.6	0	-1.5
902	TGACAGCACTTGCATCAGAA SEQ ID NO:2589	0.9	-22.7	66.4	-23	-0.3	-7
1255	TGTTGCTACACCAGCATGGT SEQ ID NO:2590	0.9	-26.4	75.3	-24.8	-2.5	-9.4
1276	CAGCTCCTCAAGAACTTGAC SEQ ID NO:2591	0.9	-23	66.9	-22.9	-0.8	-8.9
1384	TGCTGTCTCACCTGATTGAC SEQ ID NO:2592	0.9	-24.9	72.8	-25.8	0	-4.3
1389	GTATCTGCTGTCTCACCTGA SEQ ID NO:2593	0.9	-26.2	77.4	-27.1	0	-3.6
1464	ATGGAACTGCCAACTGTGTT SEQ ID NO:2594	0.9	-23.6	67.6	-23.1	-1.3	-5.4
1549	AAACTGGCTGGTATAAGCCT SEQ ID NO:2595	0.9	-23.4	66.8	-21.8	-2.5	-8.8
1849	CAAAGCCAGAGGGCCATGTT SEQ ID NO:2596	0.9	-26.6	73	-24.8	-2.7	-9.5
1921	AAGAGCATTCTGACACTTGG SEQ ID NO:2597	0.9	-21.7	64.8	-21.9	-0.4	-4.1
2127	GCAAGATTCCGTGGGAAATC SEQ ID NO:2598	0.9	-22.9	65	-22.3	-1.4	-6.5
2276	TGATATATAAATAAGGATTT SEQ ID NO:2599	0.9	-13.3	46.2	-13.6	-0.3	-5.4
2378	GATTCCAATATAGATTCCAT SEQ ID NO:2600	0.9	-20.3	60.9	-21.2	0	-2.7
2449	AAGTGGAGGGTCCAGAAATG SEQ ID NO:2601	0.9	-22.2	64.8	-21.2	-1.9	-6.2

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2685	AAAATTTTTCAGTTTTAAGT SEQ ID NO:2602	0.9	-15.1	50.6	-16	0	-6.3
2819	AAATATGTTAAGGATTGAGA SEQ ID NO:2603	0.9	-15.7	51.3	-16.6	0	-2.7
273	GTTTTGCAGGCATTGGCTTC SEQ ID NO:2604	1	-26.2	77.1	-25.7	-1.3	-9.8
364	TACATCAAATTCTATATCCA SEQ ID NO:2605	1	-18.2	56.5	-19.2	0	-3.1
2415	CTTTAAAGAAAATAATAGCT SEQ ID NO:2606	1	-13.3	45.9	-14.3	0	-7
2416	TCTTTAAAGAAAATAATAGC SEQ ID NO:2607	1	-12.8	45.1	-13	0	-9.2
2746	ATAATAGACAACAAGTCTGA SEQ ID NO:2608	1	-16.8	53.6	-16.1	-1.7	-5.7
2814	TGTTAAGGATTGAGACCCAC SEQ ID NO:2609	1	-22.5	65.4	-23	-0.2	-3.4
3030	GTGATTTTAAAGAACAAGAT SEQ ID NO:2610	1	-15.1	49.8	-16.1	0	-4.3
682	ATGAACACTTTTAAACACAA SEQ ID NO:2611	1.1	-15.6	50.2	-16.7	0	-4.4
699	ACTGCTTGCCCGGGAAAATG SEQ ID NO:2612	1.1	-25.4	67.8	-25.3	0	-10.3
1249	TACACCAGCATGGTAACTTG SEQ ID NO:2613	1.1	-22.6	65.6	-21	-2.7	-8.2
1345	ATCTCGAAAGACTGGTGTGT SEQ ID NO:2615	1.1	-22.2	65.7	-22.6	-0.4	-4.5
1474	CTCCCGTGATATGGAACTGC SEQ ID NO:2615	1.1	-25.6	70.5	-26.2	-0.2	-3.5
1842	AGAGGGCCATGTTTCAATTC SEQ ID NO:2616	1.1	-23.8	70	-24.4	0	-7.6
2110	ATCAACATCATAGCCTCTCA SEQ ID NO:2617	1.1	-23.2	68.3	-24.3	0	-3.2
2600	CTTGGCAAACCCTTCCCTAA SEQ ID NO:2618	1.1	-26.8	71.3	-27.2	-0.5	-4
2689	CAATAAAATTTTTCAGTTTT SEQ ID NO:2619	1.1	-14.6	49.1	-15.7	0	-6.7
2991	TCATTTAAAAAATAAAAGAC SEQ ID NO:2620	1.1	-9.9	39.5	-10.3	-0.5	-5
283	AATAAGCTGGGTTTTGCAGG SEQ ID NO:2621	1.2	-22.6	66.5	-22.9	-0.7	-5.2
686	GAAAATGAACACTTTTAAAC SEQ ID NO:2622	1.2	-13.2	45.5	-14.4	0	-4.4
778	GAGTATAGGAATGTGATCAG SEQ ID NO:2623	1.2	-19.2	60.2	-20.4	0	-7.4
1023	TGCACAGCTCGTCCGGGGTG SEQ ID NO:2624	1.2	-30.5	82	-31	-0.5	-7
1854	TCCACCAAAGCCAGAGGGCC SEQ ID NO:2625	1.2	-29.9	78.4	-28.4	-2.7	-6.6
2410	AAGAAAATAATAGCTAGAAT SEQ ID NO:2626	1.2	-12.8	44.9	-14	0	-6.3
2637	AAACAAATTTCAAAATAAAT SEQ ID NO:2627	1.2	-9.6	38.9	-10.8	0	-4.5
235	TCCATCAAATCCCACACCAG SEQ ID NO:2628	1.3	-25.7	69.6	-27	0	-1.1
896	CACTTGCATCAGAAGCAAAG SEQ ID NO:2629	1.3	-20.5	60.8	-19.9	-1.9	-8.8
1113	ACGACAGACTCTGGCTGCTC SEQ ID NO:2630	1.3	-26.5	75.4	-26.9	-0.7	-6.8
1627	AAGCATGATCTCTTTGCGTC SEQ ID NO:2631	1.3	-23.4	69	-23	-1.7	-6.4

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1850	CCAAAGCCAGAGGGCCATGT SEQ ID NO:2632	1.3	-28.5	76	-27.7	-2.1	-9.5
1926	TGCTGAAGAGCATTCTGACA SEQ ID NO:2633	1.3	-22.6	66.7	-21.6	-2.3	-8.6
2290	GGAATAATTATAACTGATAT SEQ ID NO:2634	1.3	-14.3	48.1	-15.6	0	-6.2
2703	GATATAAATCCTACCAATAA SEQ ID NO:2635	1.3	-16.8	52.3	-18.1	0	-2.7
2811	TAAGGATTGAGACCCACCAA SEQ ID NO:2636	1.3	-23.2	64.8	-24	-0.2	-3.7
2892	TCTTCAAATTTAAAATCATA SEQ ID NO:2637	1.3	-13.7	47	-15	0	-5
3018	AACAAGATAAAATATGTCAT SEQ ID NO:2638	1.3	-13.7	46.7	-15	0	-3.5
285	TTAATAAGCTGGGTTTTGCA SEQ ID NO:2639	1.4	-21.2	63.5	-21.7	-0.8	-5.1
754	AAGTTTATGTTCACTCCGTA SEQ ID NO:2640	1.4	-22	65.8	-23.4	0	-3.3
756	GAAAGTTTATGTTCACTCCG SEQ ID NO:2641	1.4	-21	62.4	-22.4	0	-4.6
1542	CTGGTATAAGCCTTTGTACT SEQ ID NO:2642	1.4	-22.9	67.8	-23	-1.2	-6.2
2027	CCACTGAGTGGGGCACCTTG SEQ ID NO:2643	1.4	-28.9	79.1	-28.3	-2	-8.7
2389	TTTCTGATACAGATTCCAAT SEQ ID NO:2644	1.4	-19.8	60.4	-19.9	-1.2	-6.2
3017	ACAAGATAAAATATGTCATT SEQ ID NO:2645	1.4	-14.5	48.5	-15.9	0	-3.2
1343	CTCGAAAGACTGGTGTGTTT SEQ ID NO:2646	1.5	-22	65	-22.2	-1.2	-5.2
1551	ACAAACTGGCTGGTATAAGC SEQ ID NO:2647	1.5	-21.4	63	-22	-0.7	-5.5
2042	TGCCCTGCAAGCAGTCCACT SEQ ID NO:2648	1.5	-30.4	81.9	-31	-0.6	-9.3
2157	GATATTCCTCACTCTACAGT SEQ ID NO:2649	1.5	-23	69.5	-24.5	0	-2.8
2721	TAAGGCTAACCAAACTTAGA SEQ ID NO:2650	1.5	-18.9	56.9	-19	-1.3	-5.2
2897	TCCCATCTTCAAATTTAAAA SEQ ID NO:2651	1.5	-18	54.8	-19.5	0	-5
274	GGTTTTGCAGGCATTGGCTT SEQ ID NO:2652	1.6	-27	78	-27.1	-1.3	-9.8
1848	AAAGCCAGAGGGCCATGTTT SEQ ID NO:2653	1.6	-26	72.3	-24.9	-2.7	-9.5
2097	CCTCTCAGCACAGCAAGGTG SEQ ID NO:2654	1.6	-26.9	76.5	-27.6	-0.7	-5.2
2117	GTGGGAAATCAACATCATAG SEQ ID NO:2655	1.6	-18.9	57.8	-20	-0.2	-3.6
2288	AATAATTATAACTGATATAT SEQ ID NO:2656	1.6	-12.2	44	-13.8	0	-6.2
2357	ATTCAAAGTCCTCCACAAAT SEQ ID NO:2657	1.6	-20.9	61.1	-22.5	0	-2.5
2615	CATCTTCTCTTAAAACTTGG SEQ ID NO:2658	1.6	-18.8	58.3	-20.4	0	-2.3
2772	GCTTCCTAAATTTCTTCCAC SEQ ID NO:2659	1.6	-23.3	67.9	-24.9	0	-4.9
3015	AAGATAAAATATGTCATTCA SEQ ID NO:2660	1.6	-14.7	49.1	-16.3	0	-2.8
3016	CAAGATAAAATATGTCATTC SEQ ID NO:2661	1.6	-14.7	49.1	-16.3	0	-2.8

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1254	GTTGCTACACCAGCATGGTA SEQ ID NO:2662	1.7	-26.1	74.9	-25.1	-2.7	-9.6
1390	AGTATCTGCTGTCTCACCTG SEQ ID NO:2663	1.7	-25.6	76.3	-27.3	0	-3.6
1668	CTCAGTACTTCCTTAATCAA SEQ ID NO:2664	1.7	-20.9	63.3	-22.6	0	-5.7
1843	CAGAGGGCCATGTTTCAATT SEQ ID NO:2665	1.7	-24.1	69.6	-25.8	0	-6.8
2024	CTGAGTGGGGCACCTTGATC SEQ ID NO:2666	1.7	-27	76.9	-26.7	-2	-6.7
2156	ATATTCCTCACTCTACAGTC SEQ ID NO:2667	1.7	-22.8	69.8	-24.5	0	-2.8
2419	CATTCTTTAAAGAAAATAAT SEQ ID NO:2668	1.7	-12.1	43.6	-11.8	-0.9	-12.2
2439	TCCAGAAATGCAACACCCAG SEQ ID NO:2669	1.7	-23.9	65.6	-24.9	-0.4	-5.6
284	TAATAAGCTGGGTTTTGCAG SEQ ID NO:2670	1.8	-21.1	63.3	-22	-0.8	-5.2
366	TGTACATCAAATTCTATATC SEQ ID NO:2671	1.8	-16.7	54.3	-18.5	0	-5.9
847	GAAAAGGCAGGTTGTGCTGT SEQ ID NO:2672	1.8	-23.8	69.2	-23.4	-2.2	-5.3
1209	AAACGCCGGCATCTCTGGAT SEQ ID NO:2673	1.8	-26.3	70.4	-26.5	-0.2	-11.3
1271	CCTCAAGAACTTGACGTGTT SEQ ID NO:2674	1.8	-22.5	64.8	-23.3	-0.8	-8.9
1557	AGGGATACAAACTGGCTGGT SEQ ID NO:2675	1.8	-23.6	67.9	-25.4	0	-5.2
1656	TTAATCAAATCAGGCAGCCG SEQ ID NO:2676	1.8	-22.2	63.1	-23.2	-0.3	-9
1675	ATCCATGCTCAGTACTTCCT SEQ ID NO:2677	1.8	-26.3	76.2	-28.1	0	-5.7
2149	TCACTCTACAGTCACAGATT SEQ ID NO:2678	1.8	-22	67.5	-23.8	0	-2.8
2710	AAACTTAGATATAAATCCTA SEQ ID NO:2679	1.8	-15.1	49.7	-16	-0.7	-4.2
2740	GACAACAAGTCTGAGAAACT SEQ ID NO:2680	1.8	-18.4	56.5	-19.1	-1	-4.4
2993	AGTCATTTAAAAAATAAAAG SEQ ID NO:2681	1.8	-10.3	40.2	-12.1	0	-4.5
269	TGCAGGCATTGGCTTCCCAA SEQ ID NO:2682	1.9	-28.7	78	-28.6	-2	-10.1
695	CTTGCCCGGGAAAATGAACA SEQ ID NO:2683	1.9	-23.3	63	-24	0	-10.3
696	GCTTGCCCGGGAAAATGAAC SEQ ID NO:2684	1.9	-24.4	65.5	-25.4	0	-9.6
984	ATTCGATGGATAGAAAGACG SEQ ID NO:2685	1.9	-18.2	55.1	-20.1	0	-4.7
1238	GGTAACTTGTTCCACAAGCA SEQ ID NO:2686	1.9	-23.7	68.6	-23.6	-2	-7.3
1243	AGCATGGTAACTTGTTCCAC SEQ ID NO:2687	1.9	-23.7	69.6	-24	-1.5	-7.2
1250	CTACACCAGCATGGTAACTT SEQ ID NO:2688	1.9	-23.5	67.6	-22.7	-2.7	-8.2
1347	TCATCTCGAAAGACTGGTGT SEQ ID NO:2689	1.9	-22.1	65.3	-23.3	-0.4	-4.5
2025	ACTGAGTGGGGCACCTTGAT SEQ ID NO:2690	1.9	-26.8	75.8	-26.7	-2	-6.7
2080	GTGGAAAGCCAGCAACTGTA SEQ ID NO:2691	1.9	-23.9	68	-24.3	-1.4	-6.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2379	AGATTCCAATATAGATTCCA SEQ ID NO:2692	1.9	-20.3	61.1	-22.2	0	-2.7
47	GCACACACGAGCTTCGGTGG SEQ ID NO:2693	2	-27.5	75.1	-26.3	-3.2	-10.9
681	TGAACACTTTTAAACACAAG SEQ ID NO:2694	2	-15.6	50.4	-17.6	0	-4.4
1568	CAAACATCACAAGGGATACA SEQ ID NO:2695	2	-19.1	57.2	-21.1	0	-3.5
1669	GCTCAGTACTTCCTTAATCA SEQ ID NO:2696	2	-23.4	69.9	-25.4	0	-5.7
1674	TCCATGCTCAGTACTTCCTT SEQ ID NO:2697	2	-26.4	76.7	-28.4	0	-5.7
2426	CACCCAGCATTCTTTAAAGA SEQ ID NO:2698	2	-22.6	64.9	-23.8	0	-9.4
282	ATAAGCTGGGTTTTGCAGGC SEQ ID NO:2699	2.1	-25.1	73.2	-26.3	-0.8	-5.2
753	AGTTTATGTTCACTCCGTAC SEQ ID NO:2700	2.1	-22.9	68.8	-25	0	-3.4
790	GCCTGTTCTGTAGAGTATAG SEQ ID NO:2701	2.1	-23.4	71.7	-25.5	0	-3.2
1030	GAGTGTTTGCACAGCTCGTC SEQ ID NO:2702	2.1	-26.1	77.1	-25.5	-2.7	-9.1
1241	CATGGTAACTTGTTCCACAA SEQ ID NO:2703	2.1	-21.9	64.1	-22.4	-1.5	-7.2
1556	GGGATACAAACTGGCTGGTA SEQ ID NO:2704	2.1	-23.3	67.1	-25.4	0	-5.5
2096	CTCTCAGCACAGCAAGGTGG SEQ ID NO:2705	2.1	-26.1	75.5	-27.3	-0.7	-5.5
2384	GATACAGATTCCAATATAGA SEQ ID NO:2706	2.1	-18.3	56.9	-20.4	0	-2.7
2893	ATCTTCAAATTTAAAATCAT SEQ ID NO:2707	2.1	-14	47.6	-16.1	0	-5
685	AAAATGAACACTTTTAAACA SEQ ID NO:2708	2.2	-13.3	45.6	-15.5	0	-4.4
1244	CAGCATGGTAACTTGTTCCA SEQ ID NO:2709	2.2	-24.2	70.2	-25.5	-0.8	-6.5
1541	TGGTATAAGCCTTTGTACTG SEQ ID NO:2710	2.2	-22	65.7	-22.9	-1.2	-6.2
1553	ATACAAACTGGCTGGTATAA SEQ ID NO:2711	2.2	-19.3	58.3	-21.5	0	-5.5
2155	TATTCCTCACTCTACAGTCA SEQ ID NO:2712	2.2	-23.5	71	-25.7	0	-2.8
897	GCACTTGCATCAGAAGCAAA SEQ ID NO:2713	2.3	-22.3	64.5	-22.7	-1.9	-8.8
1465	TATGGAACTGCCAACTGTGT SEQ ID NO:2715	2.3	-23.2	66.7	-24.1	-1.3	-5.4
2291	TGGAATAATTATAACTGATA SEQ ID NO:2715	2.3	-14.3	48.1	-16.6	0	-6.2
2713	ACCAAACTTAGATATAAATC SEQ ID NO:2716	2.3	-15.4	50.1	-16.8	-0.7	-3.8
2720	AAGGCTAACCAAACTTAGAT SEQ ID NO:2717	2.3	-19.2	57.4	-20.1	-1.3	-4.6
2741	AGACAACAAGTCTGAGAAAC SEQ ID NO:2718	2.3	-17.5	54.8	-18	-1.8	-6.1
3020	AGAACAAGATAAAATATGTC SEQ ID NO:2719	2.3	-13.6	46.7	-15.9	0	-3.3
950	CTGCAACATCATCATCTTCC SEQ ID NO:2720	2.4	-23.6	68.9	-26	0	-4.9
994	AGTTCGTTTAATTCGATGGA SEQ ID NO:2721	2.4	-20.6	61.7	-22.1	-0.7	-6.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1256	GTGTTGCTACACCAGCATGG SEQ ID NO:2722	2.4	-26.4	75.3	-26.4	-2.4	-9.9
1666	CAGTACTTCCTTAATCAAAT SEQ ID NO:2723	2.4	-18.9	58	-21.3	0	-5.7
2358	TATTCAAAGTCCTCCACAAA SEQ ID NO:2724	2.4	-20.6	60.6	-23	0	-2.5
2464	TGTCTTCTCAGATTGAAGTG SEQ ID NO:2725	2.4	-20.8	64.9	-21.9	-1.2	-5.9
2990	CATTTAAAAAATAAAAGACT SEQ ID NO:2726	2.4	-10.4	40.3	-12.1	-0.5	-5
3009	AAATATGTCATTCAGCAGTC SEQ ID NO:2727	2.4	-19.9	61.9	-22.3	0	-4.1
293	CTTTCTTCTTAATAAGCTGG SEQ ID NO:2728	2.5	-19.8	61.2	-22.3	0	-5.1
1258	ACGTGTTGCTACACCAGCAT SEQ ID NO:2729	2.5	-26.2	73.4	-26.3	-2.4	-9.1
1431	GTTAAAGCTCCTCTCTCCTT SEQ ID NO:2730	2.5	-25.6	74.7	-28.1	0	-4.5
2359	TTATTCAAAGTCCTCCACAA SEQ ID NO:2731	2.5	-21.4	62.9	-23.9	0	-2.5
2894	CATCTTCAAATTTAAAATCA SEQ ID NO:2732	2.5	-14.7	48.8	-17.2	0	-5
2896	CCCATCTTCAAATTTAAAAT SEQ ID NO:2733	2.5	-17.6	53.7	-20.1	0	-5
70	GAGTGGCTGGCGGGATCGGG SEQ ID NO:2734	2.6	-30.1	80.9	-31.8	-0.7	-5.5
290	TCTTCTTAATAAGCTGGGTT SEQ ID NO:2735	2.6	-21.2	64.7	-23.8	0	-5.1
737	GTACACCAATCAACAGAGGG SEQ ID NO:2736	2.6	-22.3	64.6	-24.9	0	-4.6
1259	GACGTGTTGCTACACCAGCA SEQ ID NO:2737	2.6	-26.8	74.7	-27.2	-2.2	-9.6
1386	TCTGCTGTCTCACCTGATTG SEQ ID NO:2738	2.6	-25.4	74.6	-28	0	-3.6
1471	CCGTGATATGGAACTGCCAA SEQ ID NO:2739	2.6	-24.3	66.3	-25.5	-1.3	-5.2
1472	CCCGTGATATGGAACTGCCA SEQ ID NO:2740	2.6	-27	71.6	-28.4	-1.1	-4.8
1667	TCAGTACTTCCTTAATCAAA SEQ ID NO:2741	2.6	-19.3	59.3	-21.9	0	-5.7
2331	GAAAATGTAAGAGGTAACTT SEQ ID NO:2742	2.6	-15.9	51.4	-17.2	-1.2	-3.5
2711	CAAACTTAGATATAAATCCT SEQ ID NO:2743	2.6	-16.1	51.4	-17.9	-0.6	-4.2
898	AGCACTTGCATCAGAAGCAA SEQ ID NO:2744	2.7	-23	66.9	-24.1	-1.5	-8.3
1385	CTGCTGTCTCACCTGATTGA SEQ ID NO:2745	2.7	-25.6	74.2	-28.3	0	-3.6
2031	CAGTCCACTGAGTGGGGCAC SEQ ID NO:2746	2.7	-28.2	80.1	-28.6	-2.3	-10.6
2085	GCAAGGTGGAAAGCCAGCAA SEQ ID NO:2747	2.7	-24.9	68.8	-26	-1.6	-6.9
2150	CTCACTCTACAGTCACAGAT SEQ ID NO:2748	2.7	-22.8	69.2	-25.5	0	-2.8
2420	GCATTCTTTAAAGAAAATAA SEQ ID NO:2749	2.7	-13.9	47.1	-14.6	-0.9	-12.2
2987	TTAAAAAATAAAAGACTACA SEQ ID NO:2750	2.7	-10.2	40	-12.9	0	-2.2
2994	CAGTCATTTAAAAAATAAAA SEQ ID NO:2751	2.7	-11	41.4	-13	-0.5	-5

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
351	ATATCCAAATCCATATCTTG SEQ ID NO:2752	2.8	-19.6	59	-22.4	0	-2.4
1342	TCGAAAGACTGGTGTGTTTC SEQ ID NO:2753	2.8	-21.5	64.5	-21.9	-2.4	-4.9
1687	CTGAATTTCGTCATCCATGC SEQ ID NO:2754	2.8	-23.4	67.4	-26.2	0	-5
2111	AATCAACATCATAGCCTCTC SEQ ID NO:2755	2.8	-21.8	64.9	-24.6	0	-3.2
2417	TTCTTTAAAGAAAATAATAG SEQ ID NO:2756	2.8	-11.1	41.9	-12.3	-0.4	-11.2
2447	GTGGAGGGTCCAGAAATGCA SEQ ID NO:2757	2.8	-25.4	72.1	-26.3	-1.9	-8.7
2448	AGTGGAGGGTCCAGAAATGC SEQ ID NO:2758	2.8	-24.7	71.2	-25.6	-1.9	-6.2
64	CTGGCGGGATCGGGGGTGCA SEQ ID NO:2759	2.9	-31.4	82.8	-33.4	-0.7	-6.8
679	AACACTTTTAAACACAAGTG SEQ ID NO:2760	2.9	-16.2	51.8	-16.9	-2.2	-8.4
738	CGTACACCAATCAACAGAGG SEQ ID NO:2761	2.9	-21.9	62.5	-24.8	0	-4.8
2475	TAGAAACATATTGTCTTCTC SEQ ID NO:2762	2.9	-17.9	57.4	-19.1	-1.7	-6.3
2714	AACCAAACTTAGATATAAAT SEQ ID NO:2763	2.9	-14.3	47.5	-16.3	-0.7	-3
260	TGGCTTCCCAATCTTTATCA SEQ ID NO:2764	3	-24.7	70.8	-26.8	-0.8	-3.7
275	GGGTTTTGCAGGCATTGGCT SEQ ID NO:2765	3	-28.1	80.3	-29.6	-1.3	-9.8
1257	CGTGTTGCTACACCAGCATG SEQ ID NO:2766	3	-26	72.6	-26.9	-2.1	-6
1481	AATCTGTCTCCCGTGATATG SEQ ID NO:2767	3	-23.8	68.3	-26.8	0	-3.3
1927	TTGCTGAAGAGCATTCTGAC SEQ ID NO:2768	3	-22	65.8	-22.5	-2.5	-8.8
2647	AACAAAACAGAAACAAATTT SEQ ID NO:2769	3	-11.9	42.8	-14.9	0	-4.3
2742	TAGACAACAAGTCTGAGAAA SEQ ID NO:2770	3	-17	53.8	-18	-2	-6.8
1341	CGAAAGACTGGTGTGTTTCT SEQ ID NO:2771	3.1	-22	65	-21.9	-3.2	-6.4
2388	TTCTGATACAGATTCCAATA SEQ ID NO:2772	3.1	-19.4	59.5	-21.2	-1.2	-6.2
2743	ATAGACAACAAGTCTGAGAA SEQ ID NO:2773	3.1	-17.7	55.6	-18.8	-2	-6.8
2754	ACCTACAGATAATAGACAAC SEQ ID NO:2774	3.1	-18	55.6	-21.1	0	-2.4
745	TTCACTCCGTACACCAATCA SEQ ID NO:2775	3.2	-24.6	68.9	-27.8	0	-4.8
755	AAAGTTTATGTTCACTCCGT SEQ ID NO:2776	3.2	-21.6	64.2	-24.8	0	-3.7
1475	TCTCCCGTGATATGGAACTG SEQ ID NO:2777	3.2	-24.2	68	-26.9	-0.2	-3.5
1938	CGAGCAACCACTTGCTGAAG SEQ ID NO:2778	3.2	-23.9	66.3	-23.5	-3.6	-8.4
2434	AAATGCAACACCCAGCATTC SEQ ID NO:2779	3.2	-23.2	64.9	-23.3	-3.1	-8.4
2808	GGATTGAGACCCACCAATGC SEQ ID NO:2780	3.2	-26	70.9	-28.3	-0.7	-4.1
771	GGAATGTGATCAGTAGAAAG SEQ ID NO:2781	3.3	-18.1	56.7	-21.4	0	-6.6

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
798	TTGTCTTTGCCTGTTCTGTA SEQ ID NO:2782	3.3	-25	75.4	-28.3	0	-3
813	TTGCAGCTTCCTTTCTTGTC SEQ ID NO:2783	3.3	-25.9	77.5	-29.2	0	-5.2
901	GACAGCACTTGCATCAGAAG SEQ ID NO:2784	3.3	-22.7	66.8	-25.1	-0.7	-7
1430	TTAAAGCTCCTCTCTCCTTA SEQ ID NO:2785	3.3	-24.1	70.6	-27.4	0	-5
1470	CGTGATATGGAACTGCCAAC SEQ ID NO:2786	3.3	-22.5	63.5	-24.4	-1.3	-5.2
2719	AGGCTAACCAAACTTAGATA SEQ ID NO:2787	3.3	-19.6	58.7	-21.5	-1.3	-4.4
2732	GTCTGAGAAACTAAGGCTAA SEQ ID NO:2788	3.3	-19.3	58.9	-22.6	0	-3.7
2988	TTTAAAAAATAAAAGACTAC SEQ ID NO:2789	3.3	-9.6	39	-12.9	0	-4
1844	CCAGAGGGCCATGTTTCAAT SEQ ID NO:2790	3.4	-26	72.8	-28.9	0	-7.6
1937	GAGCAACCACTTGCTGAAGA SEQ ID NO:2791	3.4	-23.7	67.3	-23.5	-3.6	-8.4
2114	GGAAATCAACATCATAGCCT SEQ ID NO:2792	3.4	-21.2	61.9	-24.6	0	-3.2
2646	ACAAAACAGAAACAAATTTC SEQ ID NO:2793	3.4	-13	45	-15	-1.3	-4.5
2648	AAACAAAACAGAAACAAATT SEQ ID NO:2794	3.4	-11.1	41.3	-14.5	0	-2.9
291	TTCTTCTTAATAAGCTGGGT SEQ ID NO:2795	3.5	-21.2	64.7	-24.7	0	-5.1
2712	CCAAACTTAGATATAAATCC SEQ ID NO:2796	3.5	-17.2	53.2	-19.8	-0.7	-4.2
2745	TAATAGACAACAAGTCTGAG SEQ ID NO:2797	3.5	-16.8	53.7	-18.3	-2	-5.7
281	TAAGCTGGGTTTTGCAGGCA SEQ ID NO:2798	3.6	-25.8	74.3	-28.5	-0.8	-5.9
899	CAGCACTTGCATCAGAAGCA SEQ ID NO:2799	3.6	-24.4	70.3	-27.1	-0.8	-7.5
993	GTTCGTTTAATTCGATGGAT SEQ ID NO:2800	3.6	-20.6	61.5	-23.3	-0.7	-6.3
1350	ACATCATCTCGAAAGACTGG SEQ ID NO:2801	3.6	-20.6	61	-23.5	-0.4	-4.5
2639	AGAAACAAATTTCAAAATAA SEQ ID NO:2802	3.6	-10.9	41.2	-12.1	-2.4	-5.6
3012	ATAAAATATGTCATTCAGCA SEQ ID NO:2803	3.6	-17.3	54.7	-20.9	0	-4.1
3029	TGATTTTAAAGAACAAGATA SEQ ID NO:2804	3.6	-13.6	46.7	-17.2	0	-4.6
812	TGCAGCTTCCTTTCTTGTCT SEQ ID NO:2805	3.7	-26.7	79.2	-30.4	0	-4.9
1239	TGGTAACTTGTTCCACAAGC SEQ ID NO:2806	3.7	-23	67.3	-23.8	-2.9	-8.2
1476	GTCTCCCGTGATATGGAACT SEQ ID NO:2807	3.7	-25.4	71.3	-29.1	0	-3.5
2033	AGCAGTCCACTGAGTGGGGC SEQ ID NO:2808	3.7	-29.1	83.5	-30.5	-2.3	-10.6
2113	GAAATCAACATCATAGCCTC SEQ ID NO:2809	3.7	-20.4	60.8	-24.1	0	-3.2
2381	ACAGATTCCAATATAGATTC SEQ ID NO:2810	3.7	-18.5	57.8	-22.2	0	-2.7
2807	GATTGAGACCCACCAATGCA SEQ ID NO:2811	3.7	-25.5	69.5	-28.3	-0.7	-5.5

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1346	CATCTCGAAAGACTGGTGTG SEQ ID NO:2812	3.8	-21.7	63.8	-24.8	-0.4	-4.5
1348	ATCATCTCGAAAGACTGGTG SEQ ID NO:2813	3.8	-20.9	62.2	-24	-0.4	-4.5
1432	AGTTAAAGCTCCTCTCTCCT SEQ ID NO:2815	3.8	-25.5	74.6	-29.3	0	-5
1469	GTGATATGGAACTGCCAACT SEQ ID NO:2815	3.8	-22.6	65	-25	-1.3	-5.2
1661	CTTCCTTAATCAAATCAGGC SEQ ID NO:2816	3.8	-21.2	62.8	-25	0	-3.2
2158	AGATATTCCTCACTCTACAG SEQ ID NO:2817	3.8	-21.8	66.3	-25.6	0	-2.8
3010	AAAATATGTCATTCAGCAGT SEQ ID NO:2818	3.8	-18.8	58.4	-22.6	0	-4.1
794	CTTTGCCTGTTCTGTAGAGT SEQ ID NO:2819	3.9	-25.1	75.4	-29	0	-3.2
1240	ATGGTAACTTGTTCCACAAG SEQ ID NO:2820	3.9	-21.2	63.1	-22.4	-2.7	-7.9
1251	GCTACACCAGCATGGTAACT SEQ ID NO:2821	3.9	-25.2	71.4	-26.6	-2.5	-8.2
1567	AAACATCACAAGGGATACAA SEQ ID NO:2822	3.9	-17.7	54.3	-21.6	0	-3.5
2116	TGGGAAATCAACATCATAGC SEQ ID NO:2823	3.9	-19.5	58.8	-23.4	0	-2.9
2154	ATTCCTCACTCTACAGTCAC SEQ ID NO:2824	3.9	-24	72.3	-27.9	0	-2.8
357	AATTCTATATCCAAATCCAT SEQ ID NO:2825	4	-18.9	57.2	-22.9	0	-2.4
1417	CTCCTTACAGTAACGAAGAC SEQ ID NO:2826	4	-20.8	61.4	-24.8	0	-4.7
1660	TTCCTTAATCAAATCAGGCA SEQ ID NO:2827	4	-21	62.1	-25	0	-4
2047	GAGAATGCCCTGCAAGCAGT SEQ ID NO:2828	4	-26.7	73.7	-29.8	-0.5	-9.3
2151	CCTCACTCTACAGTCACAGA SEQ ID NO:2829	4	-24.8	73.1	-28.8	0	-2.8
797	TGTCTTTGCCTGTTCTGTAG SEQ ID NO:2830	4.1	-24.9	75.3	-29	0	-3
1673	CCATGCTCAGTACTTCCTTA SEQ ID NO:2831	4.1	-25.7	74.3	-29.8	0	-5.7
2387	TCTGATACAGATTCCAATAT SEQ ID NO:2832	4.1	-19.3	59.2	-22.4	-0.9	-5.7
2438	CCAGAAATGCAACACCCAGC SEQ ID NO:2833	4.1	-25.3	68	-28.7	-0.4	-5.6
2643	AAACAGAAACAAATTTCAAA SEQ ID NO:2834	4.1	-12.1	43.2	-14.6	-1.6	-4.7
3011	TAAAATATGTCATTCAGCAG SEQ ID NO:2835	4.1	-17.3	54.9	-21.4	0	-4.1
268	GCAGGCATTGGCTTCCCAAT SEQ ID NO:2836	4.2	-28.7	78.2	-30.3	-2.6	-8.9
952	TGCTGCAACATCATCATCTT SEQ ID NO:2837	4.2	-23	67.7	-27.2	0	-7.1
985	AATTCGATGGATAGAAAGAC SEQ ID NO:2838	4.2	-16.7	52.6	-20.9	0	-4.7
1355	AGCAAACATCATCTCGAAAG SEQ ID NO:2839	4.2	-18.8	56.6	-23	0	-4.5
1401	AGACCCATCAAAGTATCTGC SEQ ID NO:2840	4.2	-23.2	67.1	-26.7	-0.4	-3
1480	ATCTGTCTCCCGTGATATGG SEQ ID NO:2841	4.2	-25.7	73.2	-29.9	0	-3.1

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
2030	AGTCCACTGAGTGGGGCACC SEQ ID NO:2842	4.2	-29.5	82.7	-31.4	-2.3	-10.6
2649	AAAACAAAACAGAAACAAAT SEQ ID NO:2843	4.2	-10.3	39.9	-14.5	0	-0.9
3040	GCTCTGTGTTGTGATTTTAA SEQ ID NO:2844	4.2	-21.6	66.4	-25.8	0	-2.8
262	ATTGGCTTCCCAATCTTTAT SEQ ID NO:2845	4.3	-23.7	68.5	-25.4	-2.6	-6.8
356	ATTCTATATCCAAATCCATA SEQ ID NO:2846	4.3	-19.3	58.5	-23.6	0	-2.1
358	AAATTCTATATCCAAATCCA SEQ ID NO:2847	4.3	-18.2	55.4	-22.5	0	-3.1
744	TCACTCCGTACACCAATCAA SEQ ID NO:2848	4.3	-23.8	66.5	-28.1	0	-4.8
796	GTCTTTGCCTGTTCTGTAGA SEQ ID NO:2849	4.3	-25.5	77	-29.8	0	-3
1429	TAAAGCTCCTCTCTCCTTAC SEQ ID NO:2850	4.3	-24.2	70.8	-28.5	0	-5
2053	CACGCTGAGAATGCCCTGCA SEQ ID NO:2851	4.3	-28.1	74.3	-31.5	-0.8	-4.9
2810	AAGGATTGAGACCCACCAAT SEQ ID NO:2852	4.3	-23.5	65.3	-27.1	-0.5	-4.1
2821	GCAAATATGTTAAGGATTGA SEQ ID NO:2853	4.3	-17.6	55	-21.9	0	-3.5
2989	ATTTAAAAAATAAAAGACTA SEQ ID NO:2854	4.3	-9.4	38.6	-13	-0.5	-5
3021	AAGAACAAGATAAAATATGT SEQ ID NO:2855	4.3	-12.5	44.2	-16.8	0	-3.1
261	TTGGCTTCCCAATCTTTATC SEQ ID NO:2856	4.4	-24.1	70.1	-26.8	-1.7	-5
280	AAGCTGGGTTTTGCAGGCAT SEQ ID NO:2857	4.4	-26.1	74.9	-29.6	-0.8	-6
352	TATATCCAAATCCATATCTT SEQ ID NO:2858	4.4	-19.3	58.5	-23.7	0	-2.4
1381	TGTCTCACCTGATTGACTAA SEQ ID NO:2859	4.4	-22.1	65.7	-25.6	-0.7	-5.3
1851	ACCAAAGCCAGAGGGCCATG SEQ ID NO:2860	4.4	-27.5	73.4	-29.2	-2.7	-9.5
2086	AGCAAGGTGGAAAGCCAGCA SEQ ID NO:2861	4.4	-25.6	71.3	-27.6	-2.4	-6.7
2162	GTATAGATATTCCTCACTCT SEQ ID NO:2862	4.5	-21.8	67	-26.3	0	-2.8
2715	TAACCAAACTTAGATATAAA SEQ ID NO:2863	4.5	-14	47	-17.6	-0.7	-2.7
953	CTGCTGCAACATCATCATCT SEQ ID NO:2864	4.6	-23.8	69.3	-28.4	0	-7.3
1383	GCTGTCTCACCTGATTGACT SEQ ID NO:2865	4.6	-25.8	75	-29.5	-0.7	-5.3
1435	CACAGTTAAAGCTCCTCTCT SEQ ID NO:2866	4.6	-23.8	70.1	-28.4	0	-5
2435	GAAATGCAACACCCAGCATT SEQ ID NO:2867	4.6	-23.4	64.7	-25.1	-2.9	-8.2
2716	CTAACCAAACTTAGATATAA SEQ ID NO:2868	4.6	-15.6	50.3	-19.5	-0.5	-3.2
3013	GATAAAATATGTCATTCAGC SEQ ID NO:2869	4.6	-17.2	54.7	-21.8	0	-2.8
1466	ATATGGAACTGCCAACTGTG SEQ ID NO:2870	4.7	-22	63.6	-25.3	-1.3	-5.4
1554	GATACAAACTGGCTGGTATA SEQ ID NO:2871	4.7	-20.6	61.5	-24.8	-0.2	-5.5

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1839	GGGCCATGTTTCAATTCACC SEQ ID NO:2872	4.7	-26.1	73.5	-30.3	0	-7.6
2599	TTGGCAAACCCTTCCCTAAC SEQ ID NO:2873	4.7	-26.1	70	-30.1	-0.5	-4
2644	AAAACAGAAACAAATTTCAA SEQ ID NO:2874	4.7	-12.1	43.2	-14.4	-2.4	-5.5
784	TCTGTAGAGTATAGGAATGT SEQ ID NO:2875	4.8	-19.7	62.2	-24.5	0	-2.6
1382	CTGTCTCACCTGATTGACTA SEQ ID NO:2876	4.8	-23.7	69.9	-27.6	-0.7	-5.3
1657	CTTAATCAAATCAGGCAGCC SEQ ID NO:2877	4.8	-22.3	64.6	-26.6	0	-7.7
1670	TGCTCAGTACTTCCTTAATC SEQ ID NO:2878	4.8	-22.7	68.6	-27.5	0	-5.5
2731	TCTGAGAAACTAAGGCTAAC SEQ ID NO:2879	4.8	-18.3	56.5	-23.1	0	-3.7
2805	TTGAGACCCACCAATGCACT SEQ ID NO:2880	4.8	-26	70.7	-30.8	0	-5.5
2820	CAAATATGTTAAGGATTGAG SEQ ID NO:2881	4.8	-15.8	51.3	-20.6	0	-2.7
279	AGCTGGGTTTTGCAGGCATT SEQ ID NO:2882	4.9	-26.9	77.9	-30.9	-0.8	-6
795	TCTTTGCCTGTTCTGTAGAG SEQ ID NO:2883	4.9	-24.3	73.5	-29.2	0	-3.2
986	TAATTCGATGGATAGAAAGA SEQ ID NO:2884	4.9	-16.2	51.6	-21.1	0	-4.7
1246	ACCAGCATGGTAACTTGTTC SEQ ID NO:2885	4.9	-23.7	69.6	-26.1	-2.5	-8.8
1356	AAGCAAACATCATCTCGAAA SEQ ID NO:2886	4.9	-18.1	54.7	-23	0	-4.5
2755	CACCTACAGATAATAGACAA SEQ ID NO:2887	4.9	-18.5	56.3	-23.4	0	-2.4
1245	CCAGCATGGTAACTTGTTCC SEQ ID NO:2888	5	-25.5	72.7	-27.9	-2.6	-7.4
1340	GAAAGACTGGTGTGTTTCTG SEQ ID NO:2889	5	-21.2	64.5	-23.5	-2.7	-6.6
2044	AATGCCCTGCAAGCAGTCCA SEQ ID NO:2890	5	-28.6	76.9	-32.4	-1	-9.3
2725	AAACTAAGGCTAACCAAACT SEQ ID NO:2891	5	-18.2	54.6	-21.8	-1.3	-3.7
2730	CTGAGAAACTAAGGCTAACC SEQ ID NO:2892	5	-19.9	58.9	-24.4	-0.2	-3.7
1665	AGTACTTCCTTAATCAAATC SEQ ID NO:2893	5.1	-18.6	58	-23.7	0	-5.5
2043	ATGCCCTGCAAGCAGTCCAC SEQ ID NO:2894	5.1	-29.5	80	-33.5	-1	-9.1
2050	GCTGAGAATGCCCTGCAAGC SEQ ID NO:2895	5.1	-27.5	74.9	-31.5	-1	-6.2
2386	CTGATACAGATTCCAATATA SEQ ID NO:2896	5.1	-18.6	57.3	-23.7	0	-3.5
2421	AGCATTCTTTAAAGAAAATA SEQ ID NO:2897	5.1	-14.6	48.7	-17.7	-0.9	-12.2
2641	ACAGAAACAAATTTCAAAAT SEQ ID NO:2898	5.1	-12.8	44.6	-15.5	-2.4	-5.5
783	CTGTAGAGTATAGGAATGTG SEQ ID NO:2899	5.2	-19.3	60.6	-24.5	0	-2.2
2112	AAATCAACATCATAGCCTCT SEQ ID NO:2900	5.2	-20.7	61.4	-25.9	0	-3.2
2422	CAGCATTCTTTAAAGAAAAT SEQ ID NO:2901	5.2	-15.6	50.5	-19	-0.4	-11.7

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
988	TTTAATTCGATGGATAGAAA SEQ ID NO:2902	5.3	-15.8	50.9	-21.1	0	-4.7
990	CGTTTAATTCGATGGATAGA SEQ ID NO:2903	5.3	-19.2	57.8	-24.5	0	-4.7
1566	AACATCACAAGGGATACAAA SEQ ID NO:2904	5.3	-17.7	54.3	-23	0	-3.5
2046	AGAATGCCCTGCAAGCAGTC SEQ ID NO:2905	5.3	-26.5	74	-29.5	-2.2	-11.6
2425	ACCCAGCATTCTTTAAAGAA SEQ ID NO:2906	5.3	-21.2	61.7	-24.7	-0.7	-11.8
2640	CAGAAACAAATTTCAAAATA SEQ ID NO:2907	5.3	-12.3	43.7	-15.2	-2.4	-5.6
2650	AAAAACAAAACAGAAACAAA SEQ ID NO:2908	5.3	-9.6	38.8	-14.9	0	0
987	TTAATTCGATGGATAGAAAG SEQ ID NO:2909	5.4	-15.7	50.7	-21.1	0	-4.4
1275	AGCTCCTCAAGAACTTGACG SEQ ID NO:2910	5.4	-23.1	66	-27.5	-0.8	-8.9
1377	TCACCTGATTGACTAAGGAA SEQ ID NO:2911	5.4	-20.7	61.3	-25.2	-0.7	-4
1380	GTCTCACCTGATTGACTAAG SEQ ID NO:2912	5.4	-22.1	66	-27.5	0	-4.5
1479	TCTGTCTCCCGTGATATGGA SEQ ID NO:2913	5.4	-26.3	74.6	-31.2	-0.2	-3.4
2437	CAGAAATGCAACACCCAGCA SEQ ID NO:2915	5.4	-24	65.7	-28.3	-1	-5.6
2642	AACAGAAACAAATTTCAAAA SEQ ID NO:2915	5.4	-12.1	43.2	-15.1	-2.4	-5.5
746	GTTCACTCCGTACACCAATC SEQ ID NO:2916	5.5	-25.1	71	-30.6	0	-4.8
761	CAGTAGAAAGTTTATGTTCA SEQ ID NO:2917	5.5	-18.3	58.3	-23.8	0.3	-4.6
989	GTTTAATTCGATGGATAGAA SEQ ID NO:2918	5.5	-17.7	55.3	-23.2	0	-4.7
1253	TTGCTACACCAGCATGGTAA SEQ ID NO:2919	5.5	-24.2	69.2	-27	-2.7	-9
2034	AAGCAGTCCACTGAGTGGGG SEQ ID NO:2920	5.5	-26.6	76.1	-29.8	-2.3	-9.2
2147	ACTCTACAGTCACAGATTTG SEQ ID NO:2921	5.5	-21	64.8	-26.5	0	-2.8
2160	ATAGATATTCCTCACTCTAC SEQ ID NO:2922	5.5	-20.8	64.2	-26.3	0	-3.2
276	TGGGTTTTGCAGGCATTGGC SEQ ID NO:2923	5.6	-27.2	78	-31.8	-0.5	-9.6
1357	AAAGCAAACATCATCTCGAA SEQ ID NO:2924	5.6	-18.1	54.7	-23.7	0	-4.5
1478	CTGTCTCCCGTGATATGGAA SEQ ID NO:2925	5.6	-25.2	70.6	-30.3	-0.2	-3.5
1840	AGGGCCATGTTTCAATTCAC SEQ ID NO:2926	5.6	-24.1	70.1	-29.2	0	-7.6
2146	CTCTACAGTCACAGATTTGG SEQ ID NO:2927	5.6	-22	67	-27.6	0	-3.2
2161	TATAGATATTCCTCACTCTA SEQ ID NO:2928	5.6	-20.3	63	-25.9	0	-3.1
2895	CCATCTTCAAATTTAAAATC SEQ ID NO:2929	5.6	-16	51.3	-21.6	0	-5
353	CTATATCCAAATCCATATCT SEQ ID NO:2930	5.7	-20.1	60	-25.8	0	-2.4
954	ACTGCTGCAACATCATCATC SEQ ID NO:2931	5.7	-23.1	67.9	-28.8	0	-7.3

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1564	CATCACAAGGGATACAAACT SEQ ID NO:2932	5.7	-19.3	57.8	-25	0	-3.5
1565	ACATCACAAGGGATACAAAC SEQ ID NO:2933	5.7	-18.6	56.5	-24.3	0	-3.5
2729	TGAGAAACTAAGGCTAACCA SEQ ID NO:2934	5.7	-19.7	58.3	-24	-1.3	-3.8
2159	TAGATATTCCTCACTCTACA SEQ ID NO:2935	5.8	-21.5	65.5	-27.3	0	-2.8
2382	TACAGATTCCAATATAGATT SEQ ID NO:2936	5.8	-17.8	55.9	-23.6	0	-2.7
2436	AGAAATGCAACACCCAGCAT SEQ ID NO:2937	5.8	-23.3	64.6	-27.2	-1.9	-6.2
355	TTCTATATCCAAATCCATAT SEQ ID NO:2938	5.9	-19.3	58.5	-25.2	0	-2.4
781	GTAGAGTATAGGAATGTGAT SEQ ID NO:2939	5.9	-19	60	-24.9	0	-2.2
2052	ACGCTGAGAATGCCCTGCAA SEQ ID NO:2940	5.9	-26.7	71.2	-31.5	-1	-5.3
2804	TGAGACCCACCAATGCACTA SEQ ID NO:2941	5.9	-25.6	69.8	-31.5	0	-5.5
2809	AGGATTGAGACCCACCAATG SEQ ID NO:2942	5.9	-24.2	67.2	-29.2	-0.7	-3.9
779	AGAGTATAGGAATGTGATCA SEQ ID NO:2943	6	-19.2	60.2	-25.2	0	-7.2
789	CCTGTTCTGTAGAGTATAGG SEQ ID NO:2944	6	-22.8	69.8	-28.8	0	-3
1376	CACCTGATTGACTAAGGAAA SEQ ID NO:2945	6	-19.6	58.1	-24.7	-0.7	-4
1555	GGATACAAACTGGCTGGTAT SEQ ID NO:2946	6	-22.1	64.6	-28.1	0	-5.5
2035	CAAGCAGTCCACTGAGTGGG SEQ ID NO:2947	6	-26.1	74.6	-29.8	-2.3	-9.2
2115	GGGAAATCAACATCATAGCC SEQ ID NO:2948	6	-21.5	62.5	-27.5	0	-3.2
2822	TGCAAATATGTTAAGGATTG SEQ ID NO:2949	6	-17	53.7	-23	0	-4.7
3014	AGATAAAATATGTCATTCAG SEQ ID NO:2950	6	-15.4	50.9	-21.4	0	-2.8
762	TCAGTAGAAAGTTTATGTTC SEQ ID NO:2951	6.1	-18	58.4	-24.1	0	-4.6
992	TTCGTTTAATTCGATGGATA SEQ ID NO:2952	6.1	-19.1	58	-24.3	-0.7	-6.3
2986	TAAAAAATAAAAGACTACAG SEQ ID NO:2953	6.1	-10.1	39.8	-16.2	0	-2.2
760	AGTAGAAAGTTTATGTTCAC SEQ ID NO:2954	6.2	-17.8	57.5	-23.3	-0.5	-4
363	ACATCAAATTCTATATCCAA SEQ ID NO:2955	6.3	-17.8	55.2	-24.1	0	-3.1
1349	CATCATCTCGAAAGACTGGT SEQ ID NO:2956	6.3	-21.6	63.5	-27.3	-0.3	-4.5
1433	CAGTTAAAGCTCCTCTCTCC SEQ ID NO:2957	6.3	-25.3	73.7	-31.6	0	-5
743	CACTCCGTACACCAATCAAC SEQ ID NO:2958	6.4	-23.6	65.6	-30	0	-4.8
1351	AACATCATCTCGAAAGACTG SEQ ID NO:2959	6.4	-18.7	56.7	-24.4	-0.4	-4.5
2632	AATTTCAAAATAAATCACAT SEQ ID NO:2960	6.4	-12.8	44.8	-19.2	0	-4
359	CAAATTCTATATCCAAATCC SEQ ID NO:2961	6.5	-18.2	55.4	-24.7	0	-3.1

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1270	CTCAAGAACTTGACGTGTTG SEQ ID NO:2962	6.5	-20.5	61.1	-26	-0.8	-8.9
1672	CATGCTCAGTACTTCCTTAA SEQ ID NO:2963	6.5	-23	68.1	-29.5	0	-5.7
1671	ATGCTCAGTACTTCCTTAAT SEQ ID NO:2964	6.6	-22.3	66.9	-28.9	0	-5.7
1930	CACTTGCTGAAGAGCATTCT SEQ ID NO:2965	6.6	-23	67.8	-27.1	-2.5	-6.5
2026	CACTGAGTGGGGCACCTTGA SEQ ID NO:2966	6.6	-27.5	76.9	-32.1	-2	-8.2
278	GCTGGGTTTTGCAGGCATTG SEQ ID NO:2967	6.7	-26.9	77.4	-32.7	-0.7	-6
1550	CAAACTGGCTGGTATAAGCC SEQ ID NO:2968	6.7	-23.2	66.1	-27.5	-2.4	-8.5
2423	CCAGCATTCTTTAAAGAAAA SEQ ID NO:2969	6.7	-17.6	54.1	-22.3	-0.9	-12.2
2728	GAGAAACTAAGGCTAACCAA SEQ ID NO:2970	6.7	-19	56.6	-24.3	-1.3	-3.8
264	GCATTGGCTTCCCAATCTTT SEQ ID NO:2971	6.9	-26.5	74.4	-30.6	-2.8	-7.9
780	TAGAGTATAGGAATGTGATC SEQ ID NO:2972	6.9	-18.2	58.3	-25.1	0	-4
782	TGTAGAGTATAGGAATGTGA SEQ ID NO:2973	6.9	-19	60	-25.9	0	-2.2
1928	CTTGCTGAAGAGCATTCTGA SEQ ID NO:2974	6.9	-22.7	67.2	-27.1	-2.5	-7.2
2806	ATTGAGACCCACCAATGCAC SEQ ID NO:2975	6.9	-25.1	68.9	-31.5	-0.1	-5.5
362	CATCAAATTCTATATCCAAA SEQ ID NO:2976	7	-16.9	53	-23.9	0	-2.6
1936	AGCAACCACTTGCTGAAGAG SEQ ID NO:2977	7	-23.1	66.3	-27	-3.1	-7.7
2145	TCTACAGTCACAGATTTGGC SEQ ID NO:2978	7	-22.9	69.4	-29.9	0	-3.2
785	TTCTGTAGAGTATAGGAATG SEQ ID NO:2979	7.1	-18.6	59.3	-25.7	0	-3.2
1252	TGCTACACCAGCATGGTAAC SEQ ID NO:2980	7.2	-24.3	69.4	-28.8	-2.7	-9
1560	ACAAGGGATACAAACTGGCT SEQ ID NO:2981	7.2	-21.4	62.1	-28.6	0	-3.7
2049	CTGAGAATGCCCTGCAAGCA SEQ ID NO:2982	7.2	-26.4	71.9	-32.5	-1	-8.8
2631	ATTTCAAAATAAATCACATC SEQ ID NO:2983	7.2	-13.9	47.2	-21.1	0	-3.1
2726	GAAACTAAGGCTAACCAAAC SEQ ID NO:2984	7.2	-17.9	54.1	-23.7	-1.3	-3.7
263	CATTGGCTTCCCAATCTTTA SEQ ID NO:2985	7.3	-24.4	69.6	-28.9	-2.8	-7
265	GGCATTGGCTTCCCAATCTT SEQ ID NO:2986	7.3	-27.6	76.6	-32.1	-2.8	-8.7
1929	ACTTGCTGAAGAGCATTCTG SEQ ID NO:2987	7.3	-22.3	66.5	-27.1	-2.5	-6.5
747	TGTTCACTCCGTACACCAAT SEQ ID NO:2988	7.4	-24.7	69.3	-32.1	0	-4.8
1658	CCTTAATCAAATCAGGCAGC SEQ ID NO:2989	7.4	-22.3	64.6	-29.7	0	-4.1
266	AGGCATTGGCTTCCCAATCT SEQ ID NO:2990	7.5	-27.5	76.5	-32.2	-2.8	-8.7
2383	ATACAGATTCCAATATAGAT SEQ ID NO:2991	7.5	-17.7	55.6	-25.2	0	-2.7

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1563	ATCACAAGGGATACAAACTG SEQ ID NO:2992	7.6	-18.6	56.5	-26.2	0	-3.3
1375	ACCTGATTGACTAAGGAAAA SEQ ID NO:2993	7.7	-18.2	55.2	-25	-0.7	-4
2048	TGAGAATGCCCTGCAAGCAG SEQ ID NO:2994	7.7	-25.5	70.4	-32.1	-1	-9.1
1269	TCAAGAACTTGACGTGTTGC SEQ ID NO:2995	7.8	-21.4	63.2	-28.3	-0.6	-8.7
292	TTTCTTCTTAATAAGCTGGG SEQ ID NO:2996	7.9	-20.1	61.8	-28	0	-5.1
361	ATCAAATTCTATATCCAAAT SEQ ID NO:2997	8	-16.2	51.8	-24.2	0	-3.1
786	GTTCTGTAGAGTATAGGAAT SEQ ID NO:2998	8.1	-19.8	62.7	-27.9	0	-3.4
2385	TGATACAGATTCCAATATAG SEQ ID NO:2999	8.1	-17.7	55.6	-25.8	0	-2.7
1934	CAACCACTTGCTGAAGAGCA SEQ ID NO:3000	8.2	-23.8	67.2	-29.7	-2.3	-6.2
2051	CGCTGAGAATGCCCTGCAAG SEQ ID NO:3001	8.3	-26.5	70.9	-33.7	-1	-5.3
2727	AGAAACTAAGGCTAACCAAA SEQ ID NO:3002	8.3	-17.7	53.7	-24.6	-1.3	-3.7
360	TCAAATTCTATATCCAAATC SEQ ID NO:3003	8.4	-16.6	52.9	-25	0	-3.1
1360	GAAAAAGCAAACATCATCTC SEQ ID NO:3004	8.4	-16.6	52.3	-25	0	-4.1
1379	TCTCACCTGATTGACTAAGG SEQ ID NO:3005	8.4	-22.1	65.4	-30.5	0.6	-3.7
1467	GATATGGAACTGCCAACTGT SEQ ID NO:3006	8.4	-22.6	65	-29.6	-1.3	-5.2
1477	TGTCTCCCGTGATATGGAAC SEQ ID NO:3007	8.4	-24.5	69.3	-32.4	-0.2	-3.5
1664	GTACTTCCTTAATCAAATCA SEQ ID NO:3008	8.4	-19.3	59.1	-27.7	0	-4
1853	CCACCAAAGCCAGAGGGCCA SEQ ID NO:3009	8.4	-30.2	77.8	-35.9	-2.7	-7.6
1359	AAAAAGCAAACATCATCTCG SEQ ID NO:3010	8.5	-16.8	52	-25.3	0	-3.3
2744	AATAGACAACAAGTCTGAGA SEQ ID NO:3011	8.5	-17.7	55.6	-24.2	-2	-6.6
3027	ATTTTAAAGAACAAGATAAA SEQ ID NO:3012	8.5	-11.6	42.6	-20.1	0	-4.6
900	ACAGCACTTGCATCAGAAGC SEQ ID NO:3013	8.6	-23.9	69.8	-31.6	-0.7	-7
3025	TTTAAAGAACAAGATAAAAT SEQ ID NO:3015	8.6	-10.8	41	-19.4	0	-4
3026	TTTTAAAGAACAAGATAAAA SEQ ID NO:3015	8.6	-10.9	41.3	-19.5	0	-4.6
1434	ACAGTTAAAGCTCCTCTCTC SEQ ID NO:3016	8.7	-23.5	70.5	-32.2	0	-5
1852	CACCAAAGCCAGAGGGCCAT SEQ ID NO:3017	8.7	-28.2	74.6	-34.2	-2.7	-7.6
2045	GAATGCCCTGCAAGCAGTCC SEQ ID NO:3018	8.7	-28.5	77.2	-35.3	-1.8	-10.8
3028	GATTTTAAAGAACAAGATAA SEQ ID NO:3019	8.7	-12.9	45.2	-21.6	0	-4.6
1358	AAAAGCAAACATCATCTCGA SEQ ID NO:3020	8.8	-18.1	54.7	-26.9	0	-4.2
1558	AAGGGATACAAACTGGCTGG SEQ ID NO:3021	8.8	-21.7	62.8	-30.5	0	-3.8

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1562	TCACAAGGGATACAAACTGG SEQ ID NO:3022	8.8	-19.8	58.9	-28.6	0	-2.4
1935	GCAACCACTTGCTGAAGAGC SEQ ID NO:3023	8.8	-24.9	70.1	-31.4	-2.3	-7.4
1931	CCACTTGCTGAAGAGCATTC SEQ ID NO:3024	8.9	-24.1	69.5	-30.8	-2.2	-6.2
2717	GCTAACCAAACTTAGATATA SEQ ID NO:3025	8.9	-18.1	55.6	-27	0	-3.2
1468	TGATATGGAACTGCCAACTG SEQ ID NO:3026	9.1	-21.4	61.9	-29.6	-0.8	-5.2
1561	CACAAGGGATACAAACTGGC SEQ ID NO:3027	9.1	-21.2	61.5	-30.3	0	-2.8
1559	CAAGGGATACAAACTGGCTG SEQ ID NO:3028	9.3	-21.2	61.5	-30.5	0	-3.7
267	CAGGCATTGGCTTCCCAATC SEQ ID NO:3029	9.4	-27.3	75.6	-34.1	-2.6	-8.7
277	CTGGGTTTTGCAGGCATTGG SEQ ID NO:3030	9.4	-26.3	75.5	-35.7	0	-6
2153	TTCCTCACTCTACAGTCACA SEQ ID NO:3031	9.4	-24.7	73.5	-34.1	0	-2.8
1663	TACTTCCTTAATCAAATCAG SEQ ID NO:3032	9.5	-18.1	56.4	-27.6	0	-2.3
3024	TTAAAGAACAAGATAAAATA SEQ ID NO:3033	9.5	-10.4	40.3	-19.9	0	-2
2718	GGCTAACCAAACTTAGATAT SEQ ID NO:3034	9.6	-19.6	58.6	-28.5	-0.5	-3.7
2424	CCCAGCATTCTTTAAAGAAA SEQ ID NO:3035	9.7	-20.3	59.4	-28	-0.9	-12.2
1659	TCCTTAATCAAATCAGGCAG SEQ ID NO:3036	9.8	-20.9	62	-30.7	0	-4
1378	CTCACCTGATTGACTAAGGA SEQ ID NO:3037	10	-22.3	65.2	-31.4	-0.7	-4
1933	AACCACTTGCTGAAGAGCAT SEQ ID NO:3038	10.1	-23.1	66	-30.7	-2.5	-6.5
3023	TAAAGAACAAGATAAAATAT SEQ ID NO:3039	10.1	-10.3	40.1	-20.4	0	-2.4
1352	AAACATCATCTCGAAAGACT SEQ ID NO:3040	10.3	-18	55	-27.6	-0.4	-4.5
1662	ACTTCCTTAATCAAATCAGG SEQ ID NO:3041	10.3	-19.6	59.4	-29.9	0	-3.1
991	TCGTTTAATTCGATGGATAG SEQ ID NO:3042	10.5	-19	57.8	-28.8	-0.4	-5.8
2152	TCCTCACTCTACAGTCACAG SEQ ID NO:3043	10.6	-24.6	73.4	-35.2	0	-2.8
1354	GCAAACATCATCTCGAAAGA SEQ ID NO:3044	10.7	-19.4	57.6	-29.6	-0.2	-4.5
1361	GGAAAAAGCAAACATCATCT SEQ ID NO:3045	10.9	-17.4	53.5	-28.3	0	-4.1
1932	ACCACTTGCTGAAGAGCATT SEQ ID NO:3046	11	-23.9	68.6	-32.4	-2.5	-6.5
1370	ATTGACTAAGGAAAAAGCAA SEQ ID NO:3047	11.2	-15.6	50	-26.8	0	-4.1
1363	AAGGAAAAAGCAAACATCAT SEQ ID NO:3048	11.4	-15.4	49.3	-26.8	0	-4.1
1369	TTGACTAAGGAAAAAGCAAA SEQ ID NO:3049	11.4	-14.9	48.5	-26.3	0	-4.1
1362	AGGAAAAAGCAAACATCATC SEQ ID NO:3050	11.8	-16.5	51.9	-28.3	0	-4.1
3022	AAAGAACAAGATAAAATATG SEQ ID NO:3051	11.8	-10.6	40.6	-22.4	0	-2.7

position	oligo	total binding	duplex formation	Tm of Duplex	target structure	Intra-molecular oligo	Inter-Molecular oligo
1364	TAAGGAAAAAGCAAACATCA SEQ ID NO:3052	12.3	-15.1	48.8	-27.4	0	-4.1
1353	CAAACATCATCTCGAAAGAC SEQ ID NO:3053	12.5	-17.8	54.4	-29.6	-0.4	-4.5
1368	TGACTAAGGAAAAAGCAAAC SEQ ID NO:3054	12.6	-15	48.7	-27.6	0	-4.1
1367	GACTAAGGAAAAAGCAAACA SEQ ID NO:3055	13	-15.7	49.8	-28.7	0	-4.1
788	CTGTTCTGTAGAGTATAGGA SEQ ID NO:3056	13.8	-21.4	67.2	-35.2	0	-3.2
1373	CTGATTGACTAAGGAAAAAG SEQ ID NO:3057	14.2	-15.3	49.7	-29.5	0	-2.2
787	TGTTCTGTAGAGTATAGGAA SEQ ID NO:3058	14.3	-19.8	62.6	-34.1	0	-3.4
1374	CCTGATTGACTAAGGAAAAA SEQ ID NO:3059	14.4	-17.3	53.1	-31.7	0	-3.2
1366	ACTAAGGAAAAAGCAAACAT SEQ ID NO:3060	14.6	-15.1	48.7	-29.7	0	-4.1
1371	GATTGACTAAGGAAAAAGCA SEQ ID NO:3061	14.9	-16.9	52.8	-31.8	0	-4.1
1372	TGATTGACTAAGGAAAAAGC SEQ ID NO:3062	15.6	-16.2	51.5	-31.8	0	-2.8
1365	CTAAGGAAAAAGCAAACATC SEQ ID NO:3063	15.7	-15.3	49.3	-31	0	-4.1

Example 15

Western blot analysis of GFAT protein levels

[00193] Western blot analysis (immunoblot analysis) is carried out using standard methods. Cells are harvested 16-20 h after oligonucleotide treatment, washed once with PBS, suspended in Laemmli buffer (100 ul/well), boiled for 5 minutes and loaded on a 16% SDS-PAGE gel. Gels are run for 1.5 hours at 150 V, and transferred to membrane for western blotting. Appropriate primary antibody directed to GFAT is used, with a radiolabeled or fluorescently labeled secondary antibody directed against the primary antibody species. Bands are visualized using a PHOSPHORIMAGER™ (Molecular Dynamics, Sunnyvale CA).